

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 08:34:01 ; Search time 21.8636 Seconds
(without alignments)
94.378 Million cell updates/sec

Title: US-09-931-700-2

Perfect score: 76

Sequence: 1 YGGHQIYQFTDKD 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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21:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	76	100.0	13	AAW25159	Human preproadreno
2	57	75.0	31	AAW25160	Human preproadreno
3	57	75.0	31	AAW25162	Adrenomedullin pep
4	57	75.0	31	AAE09827	Human adrenomedull
5	57	75.0	40	AAW251768	Adrenomedullin pep
6	57	75.0	50	AAE09819	Rat adrenomedullin
7	57	75.0	52	AAW25110	Human adrenomedull
8	57	75.0	52	AAW251759	Adrenomedullin pep
9	57	75.0	52	AAW251765	Adrenomedullin pep

10	57	75.0	52	22	AAE09818	Human adrenomedull
11	57	75.0	52	24	ABP55104	Human adrenomedull
12	57	75.0	53	22	AAW25111	Glycine extended h
13	57	75.0	53	22	AAW25112	Glycine extended a
14	57	75.0	53	24	ABJ18665	Universal stress p
15	57	75.0	62	22	AAW25113	Linker peptide-adr
16	57	75.0	120	22	AAW25122	UspA(1-57)-(A)-(GS
17	57	75.0	120	22	AAW25123	UspA(1-56)-(DD)-(G
18	57	75.0	120	24	ABJ18669	Universal stress p
19	57	75.0	120	24	ABJ18670	Universal stress p
20	57	75.0	147	22	AAW25124	UspA(1-84)-(A)-(GS
21	57	75.0	147	24	ABJ18671	Universal stress p
22	57	75.0	170	22	AAW25114	Thioredoxin-(GS)SG
23	57	75.0	185	22	AAW25115	Human adrenomedull
24	57	75.0	185	22	AAW25116	Rat adrenomedullin
25	57	75.0	185	22	AAW25117	Human adrenomedull
26	57	75.0	185	22	AAW25118	Rat adrenomedullin
27	57	75.0	185	24	ABP72347	Adrenomedullin, in
28	57	75.0	188	22	AAW25119	Porcine adrenomedu
29	57	75.0	188	22	AAW25120	Porcine adrenomedu
30	57	75.0	206	24	ABJ18668	Universal stress p
31	51	67.1	53	22	AAW25121	Adrenomedullin pep
32	51	67.1	184	23	ABW25209	Mouse ischaemic co
33	45.5	59.9	986	22	ABW25210	Drosophila melanog
34	45	59.2	757	21	AAW25122	Arabidopsis thalia
35	45	59.2	766	21	AAW25123	Arabidopsis thalia
36	45	59.2	776	21	AAW25124	Arabidopsis thalia
37	44	57.9	514	21	AAW25125	S. lavenulae MmCA
38	44	57.9	2440	18	AAW25126	H. pylori cytoplas
39	41.5	54.6	37	22	AAW25127	Adrenomedullin pep
40	41	53.9	185	23	ABW25128	Lactococcus lactis
41	41	53.9	519	18	AAW25129	Staphylococcus aur
42	40	52.6	716	22	AAW25130	Human polypeptide,
43	40	52.6	1838	22	AAW25131	Human plexin-B2.
44	40	52.6	1849	22	ABW25132	Human plexin-B1/SE
45	40	52.6	1870	22	ABW25133	Novel human diagno

ALIGNMENTS

RESULT 1

AAW25159

ID AAW25159 standard; peptide; 13 AA.

XX AC AAW25159;

XX AC AAW25159;

XX 08-DEC-1997 (first entry)

DT Human preproadrenomedullin derived immunogen, P071.

XX Adrenomedullin; antibody; detection; diagnosis; cancer; renal; bone;
XX skin; blood related; disease; type II diabetes; preclampsia;
XX neurotransmission regulation; allergy; mast cell degranulation;
XX antibacterial; antifungal; wound repair.

OS Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..13

XX /note= "residues 122-131 of preproadrenomedullin
with Tyr-Gly-Gly attached at N-terminus"

XX Modified-site 13

XX /note= "amidated"

XX WO9707214-A1.

XX 27-FEB-1997.

XX 16-AUG-1996; 96WO-US13286.

XX 12-MAR-1996; 96US-0013172.

XX 18-AUG-1995; 95US-0002514.

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PR 30-AUG-1995; 95US-0002936.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Cuttitta F, Gray K, Hook W, Macri C, Martinez A;
XX Miller MJ, Unsworth EJ, Walsh T;
XX WPI; 1997-165298/15.
XX Human adrenomedullin peptide(s), PO70, PO71, PO72 and PAMP-20 - used
XX in the diagnosis and treatment of type II diabetes and cancer
XX Claim 1; Page 43; 106pp; English.
XX Human adrenomedullin (AM) peptides PO70, PO71, PO72 and PAMP-20
XX were used for the production of anti-AM antibodies (Ab). PO70 represents
XX preproAM amino acids (aa) 34-41 with the sequence Tyr-Tyr attached at
XX the N-terminus, PO71 represents preproAM aa 122-131 with the sequence
XX Tyr-Gly-Gly attached at the N-terminus, PO72 represents preproAM aa
XX 116-146 and PAMP-20 represents the proAM N-terminus. The Ab are useful
XX for the prevention and/or treatment of cancers, e.g. adrenal, nervous
XX system, lung, colon, ovarian and breast cancer by inhibiting cell
XX growth. They are also useful for regulating insulin secretion and blood
XX glucose metabolism and therefore for treating and/or preventing diabetes
XX type II. They may be used for the diagnosis or treatment of conditions
XX relating to pregnancy e.g. preeclampsia. The Ab are also useful
XX for the following: (i) regulating neurotransmission or neuron growth in
XX areas of the central nervous system; (ii) lessening or inhibiting mast
XX cell degranulation and hence reducing the effects of an allergic
XX response; (iii) inhibiting or preventing bacterial and fungal growth (to
XX treat infection); (iv) facilitating wound healing; and (v) promoting
XX organ and bone development.
XX Sequence 13 AA;
XX
XX Query Match 100.0%; Score 76; DB 18; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 1e-06;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 YGSHQIYQFTDKD 13
XX Db |||||
XX 1 YGSHQIYQFTDKD 13
XX
XX RESULT 2
XX AAW25160
XX ID AAW25160 standard; peptide; 31 AA.
XX AC AAW25160;
XX DT 08-DEC-1997 (first entry)
XX DE Human preproadrenomedullin derived immunogen, PO72.
XX
XX Adrenomedullin; antibody; detection; diagnosis; cancer; renal; bone;
XX skin; blood related; disease; type II diabetes; preeclampsia;
XX neurotransmission regulation; allergy; mast cell degranulation;
XX antibacterial; antifungal; wound repair.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..31
XX Modified-site 31
XX /note= "residues 116-146 of preproadrenomedullin"
XX /note= "amidated"
XX
XX WO9707214-A1.
XX
XX 27-FEB-1997.
XX
XX 16-AUG-1996; 96WO-US13286.
XX

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PR 12-MAR-1996; 96US-0013172.
PR 18-AUG-1995; 95US-0002514.
PR 30-AUG-1995; 95US-0002936.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Cuttitta F, Gray K, Hook W, Macri C, Martinez A;
XX Miller MJ, Unsworth EJ, Walsh T;
XX WPI; 1997-165298/15.
XX Human adrenomedullin peptide(s), PO70, PO71, PO72 and PAMP-20 - used
XX in the diagnosis and treatment of type II diabetes and cancer
XX Claim 1; Page 43; 106pp; English.
XX Human adrenomedullin (AM) peptides PO70, PO71, PO72 and PAMP-20
XX were used for the production of anti-AM antibodies (Ab). PO70 represents
XX preproAM amino acids (aa) 34-41 with the sequence Tyr-Tyr attached at
XX the N-terminus, PO71 represents preproAM aa 122-131 with the sequence
XX Tyr-Gly-Gly attached at the N-terminus, PO72 represents preproAM aa
XX 116-146 and PAMP-20 represents the proAM N-terminus. The Ab are useful
XX for the prevention and/or treatment of cancers, e.g. adrenal, nervous
XX system, lung, colon, ovarian and breast cancer by inhibiting cell
XX growth. They are also useful for regulating insulin secretion and blood
XX glucose metabolism and therefore for treating and/or preventing diabetes
XX type II. They may be used for the diagnosis or treatment of conditions
XX relating to pregnancy e.g. preeclampsia. The Ab are also useful
XX for the following: (i) regulating neurotransmission or neuron growth in
XX areas of the central nervous system; (ii) lessening or inhibiting mast
XX cell degranulation and hence reducing the effects of an allergic
XX response; (iii) inhibiting or preventing bacterial and fungal growth (to
XX treat infection); (iv) facilitating wound healing; and (v) promoting
XX organ and bone development.
XX
XX Query Match 75.0%; Score 57; DB 18; Length 31;
XX Best Local Similarity 100.0%; Pred. No. 0.006;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 HQIYQFTDKD 13
XX Db |||||
XX 7 HQIYQFTDKD 16
XX
XX RESULT 3
XX AAB91762
XX ID AAB91762 standard; Peptide; 31 AA.
XX AC AAB91762;
XX DT 22-JUN-2001 (first entry)
XX DE Adrenomedullin peptide (AM) SEQ ID NO:938.
XX
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
XX blood component; modification; succinimidyl; maleimido group; amino;
XX hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200069900-A2.
XX
XX 23-NOV-2000.
XX
XX 17-MAY-2000; 2000WO-US13576.
XX
XX 17-MAY-1999; 99US-0134406.
XX 10-SEP-1999; 99US-0153406.
XX 15-OCT-1999; 99US-0159783.
XX

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CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.

XX SQ Sequence 40 AA;

Query Match 75.0%; Score 57; DB 22; Length 40;
 Best Local Similarity 100.0%; Pred. No. 0.008;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
 |||||
 Db 16 HQIYQFTDKD 25

RESULT 6

AAE09819
 ID AAE09819 standard; peptide; 50 AA.

AC AAE09819;

XX 29-NOV-2001 (first entry)

DT Rat adrenomedullin peptide.

DE Rat; vasoactive peptide; calcitonin gene related peptide; CGRP;
 KW CGRP-receptor identification; adrenomedullin.

XX Rattus sp.

XX US6268474-B1.

XX 31-JUL-2001.

XX 30-APR-1998; 98US-0070504.

XX 30-APR-1998; 98US-0070504.

XX (UYCR-) UNIV CREIGHTON.

XX Smith DD, Saha S, Abel PW;

XX WPI; 2001-564216/63.

XX Vasoactive peptides useful for inhibiting calcitonin gene related
 PT peptide receptor activity -

XX Claim 5; Column 25-26; 24pp; English.

XX The invention relates to antagonists of the vasoactive peptide
 CC calcitonin gene related peptide (CGRP) and other members of the
 CC CGRP superfamily. The invention also relates to amino the terminal
 CC modifications of peptides to improve their ability to bind to a
 CC member of the CGRP-receptor super-family. CGRP antagonists are
 CC used for inhibiting CGRP activity which can be used in vitro e.g.
 CC in assays to identify and/or isolate CGRP receptors or with intact
 CC cells either in vitro or in vivo to inhibit the effect of CGRP
 CC binding to its receptor. The present sequence is rat adrenomedullin
 CC peptide.

XX SQ Sequence 50 AA;

Query Match 75.0%; Score 57; DB 22; Length 50;
 Best Local Similarity 100.0%; Pred. No. 0.01;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
 |||||
 Db 26 HQIYQFTDKD 35

RESULT 7

AAB75110
 ID AAB75110 standard; Protein; 52 AA.

XX AAB75110;

XX 31-JUL-2001 (first entry)

XX Human adrenomedullin (AM) protein.

XX Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
 KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.

XX Homo sapiens.

XX WO200127310-A1.

XX 19-APR-2001.

XX 10-OCT-2000; 2000WO-JP07023.

XX 15-OCT-1999; 99JP-0294147.

XX (SHIO) SHIONOGI & CO LTD.

XX Takimoto A, Mitsuda Y, Nakayama T, Mitsuhashi K;

XX WPI; 2001-282044/29.

DR N-PSDB; AAB19806.

XX Producing adrenomedullin useful for pharmaceutical and diagnostic
 PT application comprises producing fused adrenomedullin precursor using a
 PT recombinant host -

XX Disclosure; Page 45; 75pp; Japanese.

XX The present invention describes a method (M1) for producing
 CC adrenomedullin precursor. The method comprises: (a) producing the fused
 CC protein using a recombinant host cell; (b) restricted digestion of the
 CC fused protein by a protease followed by collection of sediment; and
 CC (c) dissolving the sediment and extracting adrenomedullin precursor.
 CC The method can be used for the production of adrenomedullin precursor
 CC for pharmaceutical and diagnostic applications. AAB19806 to AAB19866
 CC and AAB75110 to AAB75124 represent sequences which are used in the
 CC exemplification of the present invention.

XX SQ Sequence 52 AA;

Query Match 75.0%; Score 57; DB 22; Length 52;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
 |||||
 Db 28 HQIYQFTDKD 37

RESULT 8

AAB91759
 ID AAB91759 standard; Peptide; 52 AA.

XX AAB91759;

XX 22-JUN-2001 (first entry)

XX Adrenomedullin peptide (AM) SEQ ID NO:935.

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.
 OS Synthetic.

PN WO200069900-A2.

XX 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

XX 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure; Page 498; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.

XX Sequence 52 AA;

Query Match 75.0%; Score 57; DB 22; Length 52;

Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 4 HQIYQFTDKD 13

|||||

Db 28 HQIYQFTDKD 37

RESULT 9

AAB91765

ID AAB91765 standard; Peptide; 52 AA.

XX AAB91765;

XX 22-JUN-2001 (first entry)

XX Adrenomedullin peptide (AM) SEQ ID NO:941.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

OS Synthetic.

PN WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US13576.

XX 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure; Page 501; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.

XX Sequence 52 AA;

Query Match 75.0%; Score 57; DB 22; Length 52;

Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 4 HQIYQFTDKD 13

|||||

Db 27 HQIYQFTDKD 36

RESULT 10

AAE09818

ID AAE09818 standard; peptide; 52 AA.

XX AAE09818;

XX 29-NOV-2001 (first entry)

XX Human adrenomedullin peptide #1.

XX Human; vasoactive peptide; calcitonin gene related peptide; CGRP;
 KW CGRP-receptor identification; adrenomedullin.

XX Homo sapiens.

XX US6268474-B1.

XX 31-JUL-2001.

XX 30-APR-1998; 98US-0070504.

XX 30-APR-1998; 98US-0070504.
 XX (UYCR-) UNIV CREIGHTON.
 XX Smith DP, Saha S, Abel PW;
 XX WPI; 2001-564216/63.
 XX
 XX Vasoactive peptides useful for inhibiting calcitonin gene related
 XX peptide receptor activity -
 XX
 XX Claim 5; Column 25-26; 24pp; English.
 XX
 XX The invention relates to antagonists of the vasoactive peptide
 XX calcitonin gene related peptide (CGRP) and other members of the
 XX CGRP superfamily. The invention also relates to amino the terminal
 XX modifications of peptides to improve their ability to bind to a
 XX member of the CGRP-receptor super-family. CGRP antagonists are
 XX used for inhibiting CGRP activity which can be used in vitro e.g.
 XX in assays to identify and/or isolate CGRP receptors or with intact
 XX cells either in vitro or in vivo to inhibit the effect of CGRP
 XX binding to its receptor. The present sequence is human
 XX adrenomedullin peptide.
 XX
 XX Sequence 52 AA;
 XX
 XX Query Match 75.0%; Score 57; DB 22; Length 52;
 XX Best Local Similarity 100.0%; Pred. No. 0.011;
 XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 4 HQIYQFTDKD 13
 XX | | | | | | | |
 XX DB 28 HQIYQFTDKD 37
 XX
 XX RESULT 11
 XX ABP55104
 XX ID ABP55104 standard; Peptide; 52 AA.
 XX AC ABP55104;
 XX
 XX 07-FEB-2003 (first entry)
 XX Human adrenomedullin.
 XX
 XX Adrenomedullin; human; protein engineering; solubility;
 XX aggregation; hypotensive; vasodilator; cyclic.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX Disulfide-bond 16..21
 XX
 XX WO200283734-A2.
 XX
 XX 24-OCT-2002.
 XX
 XX 17-APR-2002; 2002WO-GB01778.
 XX
 XX 17-APR-2001; 2001GB-0009438.
 XX
 XX (ISIS-) ISIS INNOVATION LTD.
 XX
 XX Zurdo J, Dobson CM;
 XX
 XX WPI; 2003-046916/04.
 XX
 XX New modified human calcitonin peptide having reduced aggregation,
 XX useful for the treatment of Paget's disease, hypercalcemia and/or
 XX osteoporosis -
 XX
 XX Example; Page 21; 35pp; English.

XX
 XX The present sequence is that of human adrenomedullin, a potent
 XX hypotensive and vasodilator. The invention provides modified
 XX calcitonin and related peptides, such as adrenomedullin, that
 XX have at least 70% identity to the native form but are modified
 XX such that the tendency of the peptide to aggregate is reduced.
 XX Preferred regions for modification include those for which the
 XX peptide is polymorphic amongst different species, which increase
 XX the propensity of the peptide to form local interactions of the
 XX alpha-helical type, or which reduce the number of hydrophobic
 XX residues or increase the net charge of the peptide. When
 XX aggregation is reduced or prevented, lower doses of the drug can
 XX be used. Side-effects and undesired responses are minimised by
 XX retaining high sequence identity to the human peptide.
 XX
 XX Sequence 52 AA;
 XX
 XX Query Match 75.0%; Score 57; DB 24; Length 52;
 XX Best Local Similarity 100.0%; Pred. No. 0.011;
 XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 4 HQIYQFTDKD 13
 XX | | | | | | | |
 XX DB 28 HQIYQFTDKD 37
 XX
 XX RESULT 12
 XX AAB75111
 XX ID AAB75111 standard; Protein; 53 AA.
 XX AC AAB75111;
 XX
 XX 31-JUL-2001 (first entry)
 XX Glycine extended human adrenomedullin (AM-gly) protein.
 XX
 XX Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
 XX adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
 XX
 XX Homo sapiens.
 XX
 XX WO200127310-A1.
 XX
 XX 19-APR-2001.
 XX
 XX 10-OCT-2000; 2000WO-JP07023.
 XX
 XX 15-OCT-1999; 99JP-0294147.
 XX
 XX (SHIO) SHIONOGI & CO LTD.
 XX
 XX Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
 XX
 XX WPI; 2001-282044/29.
 XX N-PSDB; AAH19807.
 XX
 XX Producing adrenomedullin useful for pharmaceutical and diagnostic
 XX application comprises producing fused adrenomedullin precursor using a
 XX recombinant host -
 XX
 XX Example 1; Page 46; 75pp; Japanese.
 XX
 XX The present invention describes a method (M1) for producing
 XX adrenomedullin precursor. The method comprises: (a) producing the fused
 XX protein using a recombinant host cell; (b) restricted digestion of the
 XX fused protein by a protease followed by collection of sediment; and
 XX (c) dissolving the sediment and extracting adrenomedullin precursor.
 XX The method can be used for the production of adrenomedullin precursor
 XX for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
 XX and AAB75110 to AAB75124 represent sequences which are used in the
 XX exemplification of the present invention.
 XX
 XX Sequence 53 AA;

Query Match 75.0%; Score 57; DB 22; Length 53;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
 |||||
 Db 28 HQIYQFTDKD 37

RESULT 13
 AAB75112
 ID AAB75112 standard; Protein; 53 AA.
 XX
 AC AAB75112;
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Glycine extended adrenomedullin (AM-gly) protein.
 XX
 KW Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
 KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200127310-A1.
 XX
 PD 19-APR-2001.
 XX
 PF 10-OCT-2000; 2000WO-JP07023.
 XX
 PR 15-OCT-1999; 99JP-0294147.
 XX
 PA (SHIO) SHIONOGI & CO LTD.
 XX
 PI Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
 DR WPI: 2001-282044/29.
 DR N-PSDB; AAH19808.
 XX
 PT Producing adrenomedullin useful for pharmaceutical and diagnostic
 PT application comprises producing fused adrenomedullin precursor using a
 PT recombinant host -
 XX
 PS Disclosure; Page 47; 75pp; Japanese.
 XX
 CC The present invention describes a method (M1) for producing
 CC adrenomedullin precursor. The method comprises: (a) producing the fused
 CC protein using a recombinant host cell; (b) restricted digestion of the
 CC fused protein by a protease followed by collection of sediment; and
 CC (c) dissolving the sediment and extracting adrenomedullin precursor.
 CC The method can be used for the production of adrenomedullin precursor
 CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
 CC and AAB75110 to AAB75124 represent sequences which are used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 53 AA;

Query Match 75.0%; Score 57; DB 22; Length 53;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
 |||||
 Db 28 HQIYQFTDKD 37

RESULT 14
 ABJ18665
 ID ABJ18665 standard; Protein; 53 AA.
 XX
 AC ABJ18665;

XX 27-FEB-2003 (first entry)
 DT
 XX Universal stress protein A (uspA)-related protein #1.
 DE
 XX
 KW Fusion peptide; universal stress peptide; UspA; linker peptide;
 KW large scale peptide production.
 XX
 OS Unidentified.
 XX
 PN WO200283907-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 04-APR-2002; 2002WO-JP03374.
 XX
 PR 10-APR-2001; 2001JP-0111088.
 XX
 PA (SHIO) SHIONOGI & CO LTD.
 XX
 PI Mitsuda Y;
 DR WPI: 2003-067381/06.
 DR N-PSDB; ABT14525.
 XX
 PT Fusion polypeptide of Escherichia coli universal stress peptide with a
 PT target peptide, useful for efficient large scale production of the
 PT target peptide comprising expression of the fusion polypeptide followed
 PT by cleavage -
 XX
 PS Claim 4; Page 30; 49pp; Japanese.
 XX
 CC The invention comprises a novel fusion peptide which contains an
 CC Escherichia coli universal stress protein (USPA), a linker peptide and a
 CC target peptide. The fusion protein is cleavable by a protease. The fusion
 CC peptide of the invention is useful for the efficient large scale
 CC production of peptides. The present amino acid sequence represents a
 CC protein that was used in the invention.
 XX
 SQ Sequence 53 AA;

Query Match 75.0%; Score 57; DB 24; Length 53;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
 |||||
 Db 28 HQIYQFTDKD 37

RESULT 15
 AAB75113
 ID AAB75113 standard; Protein; 62 AA.
 XX
 AC AAB75113;
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Linker peptide-adrenomedullin (AM) precursor protein.
 XX
 KW Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
 KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200127310-A1.
 XX
 PD 19-APR-2001.
 XX
 PF 10-OCT-2000; 2000WO-JP07023.
 XX
 PR 15-OCT-1999; 99JP-0294147.

XX
 FA (SHIO) SHIONOGI & CO LTD.
 XX
 PI Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
 XX
 DR WPI: 2001-282044/29.
 DR N-PSDB; AAH19809.
 XX
 PT Producing adrenomedullin useful for pharmaceutical and diagnostic
 PT application comprises producing fused adrenomedullin precursor using a
 PT recombinant host -
 XX
 PS Claim 20; Page 48; 75pp; Japanese.
 XX
 CC The present invention describes a method (M1) for producing
 CC adrenomedullin precursor. The method comprises: (a) producing the fused
 CC protein using a recombinant host cell; (b) restricted digestion of the
 CC fused protein by a protease followed by collection of sediment; and
 CC (c) dissolving the sediment and extracting adrenomedullin precursor.
 CC The method can be used for the production of adrenomedullin precursor
 CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
 CC and AAB75110 to AAB75124 represent sequences which are used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 62 AA;

Query Match 75.0%; Score 57; DB 22; Length 62;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 HQIYQFTDKD 13
 |||||
 Db 37 HQIYQFTDKD 46

Search completed: October 14, 2003, 08:38:46
 Job time : 22.8636 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 14, 2003, 08:37:31 ; Search time 8.56818 Seconds
(without alignments)
64.196 Million cell updates/sec

Title: US-09-931-700-2

Perfect score: 76

Sequence: 1 YGGHQIYQFTDKD 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	76	100.0	13	4	US-09-011-922A-2
2	57	75.0	13	4	US-09-280-501-15
3	57	75.0	26	4	US-09-280-501-1
4	57	75.0	27	4	US-09-280-501-2
5	57	75.0	28	4	US-09-280-501-3
6	57	75.0	29	4	US-09-280-501-4
7	57	75.0	30	4	US-09-280-501-5
8	57	75.0	31	3	US-09-070-504-23
9	57	75.0	31	4	US-09-011-922A-3
10	57	75.0	31	4	US-09-011-922A-14
11	57	75.0	31	4	US-09-280-501-9
12	57	75.0	38	4	US-09-280-501-6
13	57	75.0	40	4	US-09-280-501-8
14	57	75.0	40	4	US-09-280-501-11
15	57	75.0	50	3	US-09-070-504-15
16	57	75.0	50	4	US-09-280-501-7
17	57	75.0	52	3	US-09-070-504-14
18	57	75.0	185	1	US-08-233-389C-1
19	57	75.0	185	2	US-08-801-863-1
20	57	75.0	185	2	US-08-486-596A-1
21	57	75.0	185	2	US-09-004-713-1
22	57	75.0	188	1	US-08-233-389C-3
23	57	75.0	188	2	US-08-801-863-3
24	57	75.0	188	2	US-08-486-596A-3
25	57	75.0	188	2	US-09-004-713-3
26	44	57.9	23	4	US-09-280-501-17
27	44	57.9	514	4	US-09-266-965-116

28 41 53.9 264 4 US-09-252-991A-19737 Sequence 19737, A
29 41 53.9 317 4 US-09-634-238-241 Sequence 241, App
30 40 52.6 157 4 US-09-252-991A-25900 Sequence 25900, A
31 39 51.3 433 4 US-09-252-991A-21838 Sequence 21838, A
32 39 51.3 686 3 US-09-368-169-8 Sequence 8, Appl
33 38.5 50.7 374 3 US-09-306-881-2 Sequence 2, Appl
34 38.5 50.7 396 4 US-09-107-532A-5962 Sequence 5962, Ap
35 38 50.0 418 4 US-09-107-532A-6073 Sequence 6073, Ap
36 37 48.7 302 4 US-09-599-360B-75 Sequence 75, Appl
37 37 48.7 1844 4 US-08-851-567B-53 Sequence 53, Appl
38 37 48.7 2504 4 US-08-851-567B-12 Sequence 12, Appl
39 36 47.4 196 3 US-07-998-289B-4 Sequence 4, Appl
40 36 47.4 231 4 US-09-107-532A-3675 Sequence 3675, Ap
41 36 47.4 291 4 US-09-252-991A-24398 Sequence 24398, A
42 36 47.4 347 3 US-09-333-423-2 Sequence 2, Appl
43 36 47.4 470 4 US-09-266-965-118 Sequence 118, App
44 36 47.4 484 4 US-09-581-831-2 Sequence 2, Appl
45 36 47.4 514 4 US-09-134-001C-4347 Sequence 4347, Ap

ALIGNMENTS

RESULT 1

US-09-011-922A-2
; Sequence 2, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
; APPLICANT: Cuttitta, Frank; Martinez, Edward
; APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
; APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
; APPLICANT: Karen; Macri, Charles
; TITLE OF INVENTION: Functional Role of
; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
; TITLE OF INVENTION: Product (PAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS WORD 97
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,922A
; FILING DATE: 17-Feb-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002,514
; FILING DATE: 18-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002,936
; FILING DATE: 30-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/013,172
; FILING DATE: 12-Mar-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13286
; FILING DATE: 16-Aug-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Leslie A. Serunian
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4202US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-8849
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: P071
; OTHER INFORMATION: YGG-PreproAM (122-131)
US-09-011-922A-2

Query Match 100.0%; Score 76; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGGHQIYQFTDKD 13
Db 1 YGGHQIYQFTDKD 13

RESULT 2
US-09-280-501-15
; Sequence 15, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
; APPLICANT: Cooper, Garth James Smith
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cornish, Jillian
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
; FILE REFERENCE: 08987-005001
; CURRENT APPLICATION NUMBER: US/09/280,501
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 08/634,562
; PRIOR FILING DATE: 1996-04-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-280-501-15

Query Match 75.0%; Score 57; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
Db 1 HQIYQFTDKD 10

RESULT 3
US-09-280-501-1
; Sequence 1, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
; APPLICANT: Cooper, Garth James Smith
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cornish, Jillian
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
; FILE REFERENCE: 08987-005001
; CURRENT APPLICATION NUMBER: US/09/280,501
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 08/634,562
; PRIOR FILING DATE: 1996-04-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-280-501-1

Query Match 75.0%; Score 57; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
Db 2 HQIYQFTDKD 11

RESULT 4
US-09-280-501-2
; Sequence 2, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
; APPLICANT: Cooper, Garth James Smith
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cornish, Jillian
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
; FILE REFERENCE: 08987-005001
; CURRENT APPLICATION NUMBER: US/09/280,501
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 08/634,562
; PRIOR FILING DATE: 1996-04-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-280-501-2

Query Match 75.0%; Score 57; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
Db 3 HQIYQFTDKD 12

RESULT 5
US-09-280-501-3
; Sequence 3, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
; APPLICANT: Cooper, Garth James Smith
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cornish, Jillian
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
; FILE REFERENCE: 08987-005001
; CURRENT APPLICATION NUMBER: US/09/280,501
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 08/634,562
; PRIOR FILING DATE: 1996-04-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-280-501-3

Query Match 75.0%; Score 57; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
Db 4 HQIYQFTDKD 13

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RESULT 6
US-09-280-501-4
; Sequence 4, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
; APPLICANT: Cooper, Garth James Smith
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cornish, Jillian
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
; TITLE OF INVENTION: ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
; FILE REFERENCE: 08987-005001
; CURRENT APPLICATION NUMBER: US/09/280,501
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 08/634,562
; PRIOR FILING DATE: 1996-04-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-280-501-4

Query Match 75.0%; Score 57; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
| | | | | | | |
DB 5 HQIYQFTDKD 14

RESULT 7
US-09-280-501-5
; Sequence 5, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
; APPLICANT: Cooper, Garth James Smith
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cornish, Jillian
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
; TITLE OF INVENTION: ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
; FILE REFERENCE: 08987-005001
; CURRENT APPLICATION NUMBER: US/09/280,501
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 08/634,562
; PRIOR FILING DATE: 1996-04-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-280-501-5

Query Match 75.0%; Score 57; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
| | | | | | | |
DB 6 HQIYQFTDKD 15

RESULT 8
US-09-070-504-23
; Sequence 23, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
; APPLICANT: Smith, Derek D.
; APPLICANT: Saha, Shankar
; APPLICANT: Abel, Peter W.
```

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; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
; TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mueeting, Raasch & Gebhardt, P.A.
; STREET: 119 No. 6268474th Fourth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/070,504
; APPLICATION NUMBER: US/09/070,504
; FILING DATE: 30-APR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 180.00020101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/305-1220
; TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-070-504-23

Query Match 75.0%; Score 57; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
| | | | | | | |
DB 7 HQIYQFTDKD 16

RESULT 9
US-09-011-922A-3
; Sequence 3, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
; APPLICANT: Cuttitta, Frank; Martinez,
; APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
; APPLICANT: J. Hook; William; Walsh, Thomas; Grey,
; APPLICANT: Karen; Macri, Charles
; TITLE OF INVENTION: Functional Role of
; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
; TITLE OF INVENTION: Product (PAMP) in Human Pathology and
; NUMBER OF SEQUENCES: 17
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS WORD 97
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,922A
; FILING DATE: 17-Feb-1998
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002,514
; FILING DATE: 18-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002,936
; FILING DATE: 30-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/013,172
; FILING DATE: 12-Mar-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13286
; FILING DATE: 16-Aug-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Leslie A. Serunian
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4202US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 3:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: P072
; OTHER INFORMATION: PreproAM(116-146)
US-09-011-922A-3

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Query Match          75.0%; Score 57; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      4 HQIYQFTDKD 13
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Db      7 HQIYQFTDKD 16

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RESULT 10
US-09-011-922A-14
; Sequence 14, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
; APPLICANT: Cuttitta, Frank; Martinez,
; APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
; APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
; APPLICANT: Karen; Macri, Charles
; TITLE OF INVENTION: Functional Role of
; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
; TITLE OF INVENTION: Product (PAMP) in human Pathology and
; TITLE OF INVENTION: Physiology
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS WORD 97
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011,922A
; FILING DATE: 17-Feb-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002,514
; FILING DATE: 18-Aug-1995
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US/60/002,936
; FILING DATE: 30-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/013,172
; FILING DATE: 12-Mar-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13286
; FILING DATE: 16-Aug-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Leslie A. Serunian
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4202US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; OTHER INFORMATION: Synthetic homolog of
; OTHER INFORMATION: two-thirds of the intact AM peptide
US-09-011-922A-14

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Query Match          75.0%; Score 57; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      4 HQIYQFTDKD 13
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Db      7 HQIYQFTDKD 16

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RESULT 11
US-09-280-501-9
; Sequence 9, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
; APPLICANT: Cooper, Garth James Smith
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cornish, Jillian
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
; FILE REFERENCE: 08987-005001
; CURRENT APPLICATION NUMBER: US/09/280,501
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 08/634,562
; PRIOR FILING DATE: 1996-04-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 31
; TYPE: PPT
; ORGANISM: Homo sapiens
US-09-280-501-9

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Query Match          75.0%; Score 57; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      4 HQIYQFTDKD 13
        |||||
Db      7 HQIYQFTDKD 16

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RESULT 12
US-09-280-501-6
; Sequence 6, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:

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; APPLICANT: Cooper, Garth James Smith
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cornish, Jillian
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
; FILE REFERENCE: 08987-005001
; CURRENT APPLICATION NUMBER: US/09/280,501
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 08/634,562
; PRIOR FILING DATE: 1996-04-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-280-501-6

Query Match 75.0%; Score 57; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
Db 14 HQIYQFTDKD 23

RESULT 13
US-09-280-501-8
; Sequence 8, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
; APPLICANT: Cooper, Garth James Smith
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cornish, Jillian
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
; FILE REFERENCE: 08987-005001
; CURRENT APPLICATION NUMBER: US/09/280,501
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 08/634,562
; PRIOR FILING DATE: 1996-04-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-280-501-8

Query Match 75.0%; Score 57; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
Db 18 HQIYQFTDKD 27

RESULT 14
US-09-280-501-11
; Sequence 11, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
; APPLICANT: Cooper, Garth James Smith
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cornish, Jillian
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
; FILE REFERENCE: 08987-005001
; CURRENT APPLICATION NUMBER: US/09/280,501
; CURRENT FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: 08/634,562

; PRIOR FILING DATE: 1996-04-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-280-501-11

Query Match 75.0%; Score 57; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
Db 16 HQIYQFTDKD 25

RESULT 15
US-09-070-504-15
; Sequence 15, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
; APPLICANT: Smith, Derek D.
; APPLICANT: Saha, Shankar
; APPLICANT: Abel, Peter W.
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
; TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mueeting, Raasch & Gebhardt, P.A.
; STREET: 119 No. 6268474th Fourth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,504
; FILING DATE: 30-APR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 180.00020101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/305-1220
; TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-070-504-15

Query Match 75.0%; Score 57; DB 3; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
Db 26 HQIYQFTDKD 35

Search completed: October 14, 2003, 08:41:21
Job time : 9.56818 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 08:40:27 ; Search time 26 Seconds
(without alignments)
80.564 Million cell updates/sec

Title: US-09-931-700-2

Perfect score: 76

Sequence: 1 YGGHIOYQFTDKD 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	76	100.0	13	9	US-09-931-700-2
2	57	75.0	31	9	US-09-931-700-3
3	57	75.0	31	9	US-09-931-700-14
4	57	75.0	31	9	US-09-813-345-23
5	57	75.0	50	9	US-09-813-345-15
6	57	75.0	52	9	US-09-813-345-14
7	57	75.0	52	15	US-10-197-954-2
8	44	57.9	514	12	US-09-953-348-116
9	44	57.9	514	15	US-10-267-255-116
10	44	57.9	833	15	US-10-027-000-2
11	41	53.9	519	8	US-08-781-986A-5230
12	39	51.3	1356	10	US-09-801-368-306
13	38	50.0	325	10	US-09-738-626-5238
14	37	48.7	161	10	US-09-738-626-6765
15	37	48.7	302	11	US-09-895-298-66

16	37	48.7	345	11	US-09-895-298-120	Sequence 120, Appl
17	37	48.7	688	12	US-10-254-074-2	Sequence 2, Appli
18	37	48.7	1844	15	US-10-242-056-53	Sequence 53, Appl
19	37	48.7	2504	9	US-09-817-514A-8	Sequence 8, Appli
20	37	48.7	2504	15	US-10-242-056-12	Sequence 12, Appl
21	36.5	48.0	451	12	US-10-355-430-32	Sequence 32, Appl
22	36	47.4	118	10	US-09-764-868-1062	Sequence 1062, Ap
23	36	47.4	118	11	US-09-955-999-71	Sequence 71, Appl
24	36	47.4	123	10	US-09-764-868-630	Sequence 630, App
25	36	47.4	143	10	US-09-764-868-1075	Sequence 1075, Ap
26	36	47.4	143	11	US-09-955-999-103	Sequence 103, App
27	36	47.4	213	9	US-09-815-242-4889	Sequence 4889, Ap
28	36	47.4	218	12	US-10-238-075-1104	Sequence 1104, Ap
29	36	47.4	231	9	US-09-815-242-10536	Sequence 10536, A
30	36	47.4	265	9	US-09-815-242-12332	Sequence 12332, A
31	36	47.4	265	9	US-09-815-242-12870	Sequence 12870, A
32	36	47.4	265	9	US-09-815-242-13144	Sequence 13144, A
33	36	47.4	433	12	US-10-137-870-6	Sequence 6, Appli
34	36	47.4	433	12	US-10-140-018-6	Sequence 6, Appli
35	36	47.4	433	12	US-10-140-021-6	Sequence 6, Appli
36	36	47.4	433	12	US-10-140-274-6	Sequence 6, Appli
37	36	47.4	433	12	US-10-140-471-6	Sequence 6, Appli
38	36	47.4	433	12	US-10-140-807-6	Sequence 6, Appli
39	36	47.4	433	12	US-10-140-922-6	Sequence 6, Appli
40	36	47.4	433	12	US-10-140-924-6	Sequence 6, Appli
41	36	47.4	433	12	US-10-140-926-6	Sequence 6, Appli
42	36	47.4	433	12	US-10-141-698-6	Sequence 6, Appli
43	36	47.4	433	12	US-10-141-702-6	Sequence 6, Appli
44	36	47.4	433	12	US-10-141-704-6	Sequence 6, Appli
45	36	47.4	433	12	US-10-142-421-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-931-700-2
; Sequence 2, Application US/09931700
; Patent No. US20020055615A1
; GENERAL INFORMATION:
; APPLICANT: CUITIITA, FRANK
; APPLICANT: MARTINEZ, ALFREDO
; APPLICANT: MILLER, MAE JEAN
; APPLICANT: UNSWORTH, EDWARD J.
; APPLICANT: HOOK, WILLIAM
; APPLICANT: WALSH, THOMAS
; APPLICANT: GREY, KAREN
; APPLICANT: MACRI, CHARLES
; TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
; TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; FILE REFERENCE: 2026-4202US4
; CURRENT APPLICATION NUMBER: US/09/931,700
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 09/011,922
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: PCT/US96/13286
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US/60/013,172
; PRIOR FILING DATE: 1996-03-12
; PRIOR APPLICATION NUMBER: US60/002,936
; PRIOR FILING DATE: 1995-08-30
; PRIOR APPLICATION NUMBER: US/60/002,514
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide,
; OTHER INFORMATION: P071, YGG-PreproAM (amino acids 122-131)

US-09-931-700-2

Query Match 100.0%; Score 76; DB 9; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGGHQIYQFTDKD 13
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 Db 1 YGGHQIYQFTDKD 13

RESULT 2

US-09-931-700-3
 ; Sequence 3, Application US/09931700
 ; Patent No. US20020055615A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CUTTITTA, FRANK
 ; APPLICANT: MARTINEZ, ALFREDO
 ; APPLICANT: MILLER, MAE JEAN
 ; APPLICANT: UNSWORTH, EDWARD J.
 ; APPLICANT: HOOK, WILLIAM
 ; APPLICANT: WALSH, THOMAS
 ; APPLICANT: GREY, KAREN
 ; APPLICANT: MACRI, CHARLES

; TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
 ; TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and
 ; TITLE OF INVENTION: Physiology
 ; FILE REFERENCE: 2026-4202US4

; CURRENT APPLICATION NUMBER: US/09/931,700

; PRIOR FILING DATE: 2001-08-16

; PRIOR APPLICATION NUMBER: 09/011,922

; PRIOR FILING DATE: 1998-02-17

; PRIOR APPLICATION NUMBER: PCT/US96/13286

; PRIOR FILING DATE: 1996-08-16

; PRIOR APPLICATION NUMBER: US/60/013,172

; PRIOR FILING DATE: 1996-03-12

; PRIOR APPLICATION NUMBER: US60/002,936

; PRIOR FILING DATE: 1995-08-30

; PRIOR APPLICATION NUMBER: US/60/002,514

; PRIOR FILING DATE: 1995-08-18

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 31

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Peptide, P072,

; OTHER INFORMATION: PreproAM (amino acids 116-146)

US-09-931-700-3

Query Match 75.0%; Score 57; DB 9; Length 31;
 Best Local Similarity 100.0%; Pred. No. 0.0065;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
 |||||
 Db 7 HQIYQFTDKD 16

RESULT 3

US-09-931-700-14
 ; Sequence 14, Application US/09931700
 ; Patent No. US20020055615A1
 ; GENERAL INFORMATION:

; APPLICANT: CUTTITTA, FRANK

; APPLICANT: MARTINEZ, ALFREDO

; APPLICANT: MILLER, MAE JEAN

; APPLICANT: UNSWORTH, EDWARD J.

; APPLICANT: HOOK, WILLIAM

; APPLICANT: WALSH, THOMAS

; APPLICANT: GREY, KAREN

; APPLICANT: MACRI, CHARLES

; TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
 ; TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and
 ; TITLE OF INVENTION: Physiology
 ; FILE REFERENCE: 2026-4202US4

; CURRENT APPLICATION NUMBER: US/09/931,700

; PRIOR FILING DATE: 2001-08-16

; PRIOR APPLICATION NUMBER: 09/011,922

; PRIOR FILING DATE: 1998-02-17

; PRIOR APPLICATION NUMBER: PCT/US96/13286

; PRIOR FILING DATE: 1996-08-16

; PRIOR APPLICATION NUMBER: US/60/013,172

; PRIOR FILING DATE: 1996-03-12

; PRIOR APPLICATION NUMBER: US60/002,936

; PRIOR FILING DATE: 1995-08-30

; PRIOR APPLICATION NUMBER: US/60/002,514

; PRIOR FILING DATE: 1995-08-18

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 14

; LENGTH: 31

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Peptide,

; OTHER INFORMATION: Synthetic homolog of AM (P072), Structural amino

; OTHER INFORMATION: acid sequence representing two-thirds of the

; OTHER INFORMATION: intact AM peptide

US-09-931-700-14

Query Match 75.0%; Score 57; DB 9; Length 31;

Best Local Similarity 100.0%; Pred. No. 0.0065;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
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Db 7 HQIYQFTDKD 16

RESULT 4

US-09-813-345-23

; Sequence 23, Application US/09813345

; Patent No. US20020068814A1

; GENERAL INFORMATION:

; APPLICANT: Smith, Derek D.

; Saha, Shankar

; Abel, Peter W.

; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Mueeting, Raasch & Gebhardt, P.A.

; STREET: 119 No. US20020068814A1th Fourth Street

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/813,345

; FILING DATE: 20-Mar-2001

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: McCormack, Myra H

; REGISTRATION NUMBER: 36,602

; REFERENCE/DOCKET NUMBER: 180.00020101

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 612/305-1220

; TELEFAX: 612/305-1228

; INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-813-345-23

Query Match 75.0%; Score 57; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.0065;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
|||||
Db 7 HQIYQFTDKD 16

RESULT 5

US-09-813-345-15

; Sequence 15, Application US/09813345

; Patent No. US20020068814A1

; GENERAL INFORMATION:

; APPLICANT: Smith, Derek D.

; Saha, Shankar

; Abel, Peter W.

; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR

; SUPERFAMILY AND METHODS OF USE

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Mueeting, Raasch & Gebhardt, P.A.

; STREET: 119 No. US20020068814A1 Fourth Street

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/813,345

; FILING DATE: 20-Mar-2001

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: McCormack, Myra H

; REGISTRATION NUMBER: 36,602

; REFERENCE/DOCKET NUMBER: 180.00020101

; TELEPHONE: 612/305-1220

; TELEFAX: 612/305-1228

; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 50 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-813-345-15

Query Match 75.0%; Score 57; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
|||||
Db 26 HQIYQFTDKD 35

RESULT 6

US-09-813-345-14

; Sequence 14, Application US/09813345
; Patent No. US20020068814A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Derek D.
; Saha, Shankar
; Abel, Peter W.
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
; SUPERFAMILY AND METHODS OF USE

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Mueeting, Raasch & Gebhardt, P.A.

; STREET: 119 No. US20020068814A1 Fourth Street

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55401

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/813,345

; FILING DATE: 20-Mar-2001

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: McCormack, Myra H

; REGISTRATION NUMBER: 36,602

; REFERENCE/DOCKET NUMBER: 180.00020101

; TELEPHONE: 612/305-1220

; TELEFAX: 612/305-1228

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 52 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-813-345-14

Query Match 75.0%; Score 57; DB 9; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
|||||
Db 28 HQIYQFTDKD 37

RESULT 7

US-10-197-954-2

; Sequence 2, Application US/10197954

; Publication No. US20030119021A1

; GENERAL INFORMATION:

; APPLICANT: K'ster, Hubert

; APPLICANT: Siddiqi, Subaib

; APPLICANT: Little, Daniel

; TITLE OF INVENTION: Capture Compounds, Collections Thereof

; AND Methods For Analyzing The Proteome And Complex

; FILE REFERENCE: 24743-2305

; CURRENT APPLICATION NUMBER: US/10/197,954

; PRIOR FILING DATE: 2002-07-16

; PRIOR APPLICATION NUMBER: 60/306,019

; PRIOR FILING DATE: 2001-07-16

; PRIOR APPLICATION NUMBER: 60/314,123

; PRIOR FILING DATE: 2001-08-21

; PRIOR APPLICATION NUMBER: 60/363,433

; PRIOR FILING DATE: 2002-03-11

; NUMBER OF SEQ ID NOS: 149

; SOFTWARE: FastSeq for Windows Version 4.0


```

; SEQ ID NO 2
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-197-954-2

Query Match          75.0%; Score 57; DB 15; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGHQIYQFTDKD 13
    |||||
Db 28 HQIYQFTDKD 37

RESULT 8
US-09-953-348-116
; Sequence 116, Application US/09953348
; Publication No. US20030134398A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, David. H
; APPLICANT: Mao, Yingqing
; APPLICANT: Varoglu, Mustafa
; APPLICANT: He, Min
; APPLICANT: Sheldon, Paul
; TITLE OF INVENTION: MITOMYCIN BIOSYNTHETIC GENE CLUSTER
; FILE REFERENCE: 600.530US1
; CURRENT APPLICATION NUMBER: US/09/953,348
; CURRENT FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: PCT/US00/06394
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/266965
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 116
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Streptomyces lavendulae
US-09-953-348-116

Query Match          57.9%; Score 44; DB 12; Length 514;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY 2 GGHQIYQFTDKD 11
    |||||
Db 66 GGHQIYQFYD 75

RESULT 9
US-10-267-255-116
; Sequence 116, Application US/10267255
; Publication No. US20030124689A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, D
; APPLICANT: Mao, Y
; APPLICANT: Varoglu, M
; APPLICANT: He, M
; APPLICANT: Sheldon, P
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
; FILE REFERENCE: 600.456US1
; CURRENT APPLICATION NUMBER: US/10/267,255
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 09/266,965
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: US 08/524,447
; PRIOR FILING DATE: 1996-08-19
; PRIOR APPLICATION NUMBER: PCT/US94/11279
; PRIOR FILING DATE: 1994-10-06
; PRIOR APPLICATION NUMBER: US 08/133,963
; PRIOR FILING DATE: 1993-10-07
; NUMBER OF SEQ ID NOS: 145

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 116
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Streptomyces lavendulae
US-10-267-255-116

Query Match          57.9%; Score 44; DB 15; Length 514;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 2; Indels 2; Gaps 0;

QY 2 GGHQIYQFTDKD 11
    |||||
Db 66 GGHQIYQFYD 75

RESULT 10
US-10-027-000-2
; Sequence 2, Application US/10027000
; Publication No. US20030119006A1
; GENERAL INFORMATION:
; APPLICANT: Dunn-Coleman, Nigel
; APPLICANT: Goedegebuur, Frits
; APPLICANT: Ward, Michael
; APPLICANT: Yao, Jian
; TITLE OF INVENTION: BGL4 Beta-Glucosidase and Nucleic Acids
; FILE REFERENCE: GC696
; CURRENT APPLICATION NUMBER: US/10/027,000
; CURRENT FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Trichoderma reesei
US-10-027-000-2

Query Match          57.9%; Score 44; DB 15; Length 833;
Best Local Similarity 53.8%; Pred. No. 34;
Matches 7; Conservative 3; Mismatches 3; Indels 3; Gaps 0;

QY 1 YGGHQIYQFTDKD 13
    |||||
Db 682 YVGRIYEFADKD 694

RESULT 11
US-08-781-986A-5230
; Sequence 5230, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

```

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; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 5230:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 519 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-781-986A-5230

Query Match 53.9%; Score 41; DB 8; Length 519;
Best Local Similarity 66.7%; Pred. No. 67;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGHIYQFTDKD 13
   |||||
Db 454 GGRIGQFSSKD 465

RESULT 12
US-09-801-368-306
; Sequence 306, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250Alman, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; FILE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; CURRENT APPLICATION NUMBER: US/09/801,368
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 306
; LENGTH: 1356
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-306

Query Match 51.3%; Score 39; DB 10; Length 1356;
Best Local Similarity 62.5%; Pred. No. 4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 HOIYQFTD 11
   |::|||
Db 496 HEVIEFTD 503

RESULT 13
US-09-738-626-5238
; Sequence 5238, Application US/09738626
; Publication No. US20020197605A1

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; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 5238
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5238

Query Match 50.0%; Score 38; DB 10; Length 325;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGHIYQFTDKD 13
   ||::|||
Db 13 GGPEVLEFDTTD 24

RESULT 14
US-09-738-626-6765
; Sequence 6765, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6765
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6765

Query Match 48.7%; Score 37; DB 10; Length 161;
Best Local Similarity 63.8%; Pred. No. 93;

```

Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 GHQIYQFTDKD 13
 ||:| |||
 Db 62 GHRISNTTDK 72

RESULT 15

US-09-895-298-66
 ; Sequence 66, Application US/09895298
 ; Publication No. US20030078405A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 47 Human Secreted Proteins
 ; FILE REFERENCE: P2035P1
 ; CURRENT APPLICATION NUMBER: US/09/895,298
 ; CURRENT FILING DATE: 2001-07-02
 ; PRIOR APPLICATION NUMBER: 09/591,16
 ; PRIOR FILING DATE: 2000-06-09
 ; PRIOR APPLICATION NUMBER: PCT/US99/29950
 ; PRIOR FILING DATE: 1999-12-16
 ; PRIOR APPLICATION NUMBER: 60/113,006
 ; PRIOR FILING DATE: 1998-12-18
 ; PRIOR APPLICATION NUMBER: 60/112,809
 ; PRIOR FILING DATE: 1998-12-17
 ; NUMBER OF SEQ ID NOS: 231
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 66
 ; LENGTH: 302
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (237)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-09-895-298-66

Query Match 48.7%; Score 37; DB 11; Length 302;
 Best Local Similarity 50.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGGHQIYQFTDK 12
 ||:| ||:
 Db 176 YPGIQQVYTFER 187

Search completed: October 14, 2003, 08:53:16
 Job time : 26 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 08:36:56 ; Search time 7.38636 Seconds
(without alignments)
169.257 Million cell updates/sec

Title: US-09-931-700-2
Perfect score: 76
Sequence: 1 YGGHQIYQFTBKD 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	75.0	185	2 JN0684	adrenomedullin pre
2	57	75.0	185	2 JN0766	adrenomedullin pre
3	57	75.0	188	2 S41600	adrenomedullin - p
4	51	67.1	643	2 S76069	hypothetical prote
5	45	59.2	776	2 T02702	hypothetical prote
6	44	57.9	2231	2 D71870	hypothetical prote
7	42	55.3	280	2 H70089	hypothetical prote
8	42	55.3	324	2 A87544	hypothetical prote
9	42	55.3	350	2 T21106	hypothetical prote
10	42	55.3	563	2 T09378	hypothetical prote
11	41	53.9	185	2 C86705	hypothetical prote
12	41	53.9	467	2 T21690	hypothetical prote
13	41	53.9	514	2 D89775	hypothetical prote
14	40	52.6	146	2 G83445	conserved hypother
15	40	52.6	260	2 H71979	probable type II r
16	40	52.6	275	2 T32005	hypothetical prote
17	39.5	52.0	606	2 T40556	hypothetical prote
18	39	51.3	176	2 B35697	transcription fact
19	39	51.3	310	2 H69986	hypothetical prote
20	39	51.3	444	1 F69130	histidine-tRNA lig
21	39	51.3	705	2 JX0194	prolyl oligopeptid
22	39	51.3	1356	2 S51389	ROM2 protein - yea
23	38.5	50.7	322	2 T22410	hypothetical prote
24	38	50.0	165	2 F69819	conserved hypother
25	38	50.0	254	2 H70860	probable enoyl-CoA
26	38	50.0	257	2 AH0859	periplasmic fibri
27	38	50.0	284	2 T23866	hypothetical prote
28	38	50.0	387	2 T28402	ORF MSV241 leucine
29	38	50.0	391	2 H89859	hypothetical prote

ALIGNMENTS

RESULT 1

JN0684
adrenomedullin precursor - human
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000
C:Accession: JC2351; JN0684; PN0548; JN0476
R:Kitamura, K.; Sakata, J.; Kangawa, K.; Hino, J.; Matsuo, K.; Kitamura, K.; Eto,
R.; Ishimitsu, T.; Kojima, M.; Kangawa, K.; Hino, J.; Matsuo, K.; Kitamura, K.; Eto,
Biochem. Biophys. Res. Commun. 203, 631-639, 1994
A:Title: Genomic structure of human adrenomedullin gene.
A:Reference number: JC2351; MUID:94354869; PMID:8074714
A:Accession: JC2351
A:Molecule type: DNA
A:Residues: 1-185 <JSH>
A:Cross-references: GB:S73906; NID:g765329; PIDN:AAC60642.1; PID:g765330
R:Kitamura, K.; Sakata, J.; Kangawa, K.; Kojima, M.; Matsuo, H.; Eto, T.
Biochem. Biophys. Res. Commun. 194, 720-725, 1993
A:Title: Cloning and characterization of cDNA encoding a precursor for human adrenome
A:Reference number: JN0684; MUID:93343928; PMID:7688224
A:Accession: JN0684
A:Molecule type: mRNA
A:Residues: 1-185 <KIT>
A:Cross-references: GB:D14874; NID:g455470; PIDN:BAA03589.1; PID:g500612
A:Accession: PN0548
A:Molecule type: protein
A:Residues: 22-41 <KL2>
R:Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Nakamura, S.; Matsuo, H.; Eto,
Biochem. Biophys. Res. Commun. 192, 553-560, 1993
A:Title: Adrenomedullin: A novel hypotensive peptide isolated from human pheochromocy
A:Reference number: JN0476; MUID:93249425; PMID:8387282
A:Accession: JN0476
A:Molecule type: protein
A:Residues: 95-146 <KL3>
A:Experimental source: pheochromocytoma
C:Genetics:
A:Gene: GDB:ADM
A:Cross-references: GDB:217070; OMIM:103275
A:Map position: lppter-llqter
C:Keywords: amidated carboxyl end; blood pressure control; hormone
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-185/Product: proadrenomedullin #status predicted <PBU>
F:22-41/Domain: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
F:95-146/Product: adrenomedullin #status experimental <MAT>
F:147-185/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F:41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following
F:110-115/Disulfide bonds: #status experimental
F:146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following
Query Match 75.0%; Score 57; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GHIYQFTDKD 13
|||||
Db 122 GHIYQFTDKD 131

RESULT 2

JN0766
adrenomedullin precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 11-Jul-1997
C:Accession: JN0766; PN0610
R:Sakata, J.; Shimokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, T.
Biochem. Biophys. Res. Commun. 195, 921-927, 1993
A:Title: Molecular cloning and biological activities of rat adrenomedullin, a hypotensive peptide
A:Reference number: JN0766; MUID:93384621; PMID:7690563
A:Accession: JN0766
A:Molecule type: mRNA
A:Residues: 1-185 <SAK>
A:Accession: PN0610
A:Molecule type: protein
A:Residues: 22-41 <SA2>
C:Comment: This precursor contains a unique 20-amino acid sequence designated proadrenomedullin.

C:Keywords: amidated carboxyl end
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-185/Product: proadrenomedullin #status predicted <PEU>
F:22-41/Product: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
F:94-143/Product: adrenomedullin #status predicted <MAT>
F:41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following glycosylation)
F:143/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following glycosylation)

Query Match 75.0%; Score 57; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GHIYQFTDKD 13
|||||
Db 119 GHIYQFTDKD 128

RESULT 3

S41600
adrenomedullin - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C:Accession: S41600
R:Kitamura, K.; Kangawa, K.; Kojima, M.; Ichiki, Y.; Matsuo, H.; Eto, T.
FEBS Lett. 338, 306-310, 1994
A:Title: Complete amino acid sequence of porcine adrenomedullin and cloning of cDNA encoding the gene
A:Reference number: S41600; MUID:94139945; PMID:8043068
A:Accession: S41600
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-188 <KIT>
A:Cross-references: GB:D14875; NID:g439721; PIDN:BAA03590.1; PID:g496379

Query Match 75.0%; Score 57; DB 2; Length 188;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GHIYQFTDKD 13
|||||
Db 122 GHIYQFTDKD 131

RESULT 4

S76069
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S76069

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O.; K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis S.
S:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76069
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-643 <KAN>
A:Cross-references: EMBL:D63999; GB:AE001339; NID:g1001396; PIDN:BAA10047.1; PID:d101
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 67.1%; Score 51; DB 2; Length 643;
Best Local Similarity 72.7%; Pred. No. 0.61;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GHIYQFTDKD 13
|||||
Db 447 GHIYQFTDKD 457

RESULT 5

T02702
hypothetical protein At2g03240 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein T18E12.9
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Feb-2001
C:Accession: T02702; A84446
R:Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, M.; submitted to the EMBL Data Library, September 1998
A:Description: Arabidopsis thaliana chromosome II BAC T18E12 genomic sequence.
A:Reference number: Z14702
A:Accession: T02702
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-776 <ROU>
A:Cross-references: EMBL:AC005313; NID:g3548797; PID:g3548806
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: A84446
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-776 <STO>
A:Cross-references: GB:AE002093; NID:g3548806; PIDN:AAC34478.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g03240
A:Map position: 2
A:Introns: 219/1; 340/2; 387/1; 417/2; 503/3; 538/3; 603/3; 698/3; 744/2
A:Note: T18E12.9

Query Match 59.2%; Score 45; DB 2; Length 776;
Best Local Similarity 66.7%; Pred. No. 8.6;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GHIYQFTDKD 13
|||||
Db 84 GGHQIGHFSDSD 95

RESULT 6

D71870
hypothetical protein jhp0928 - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999
C:Accession: D71870
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.

Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
 Nature 397, 176-180, 1999
 A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
 A:Reference number: A71800; MUID:99120557; PMID:9923682
 A:Accession: D71870
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-2231 <ARN>
 A:Cross-references: GB:AB001522; GB:AB001439; NID:94155505; PIDN:AA06506.1; PID:9415550
 A:Experimental source: strain J99
 C:Genetics:
 A:Gene: jhp0928

Query Match 57.9%; Score 44; DB 2; Length 2231;
 Best Local Similarity 53.8%; Pred. No. 40;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YGGHQIYQFTDKD 13
 Db 620 YGNHKIYSSNDKE 632

RESULT 7
 H70089
 hypothetical protein yycI - Bacillus subtilis
 C:Species: Bacillus subtilis
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
 C:Accession: H70089
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
 C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
 A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
 Koetter, P.; Koningsstein, G.; Kroch, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
 A:Authors: Schleich, S.; Schroter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, K.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: H70089
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-280 <KUN>
 A:Cross-references: GB:299124; GB:AL009126; NID:92636442; PIDN:CAB16075.1; PID:g2636585
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yycI
 C:Superfamily: Bacillus subtilis hypothetical protein yycI

Query Match 55.3%; Score 42; DB 2; Length 280;
 Best Local Similarity 72.7%; Pred. No. 9.7;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGGHQIYQFTD 11
 Db 152 YEGHYIQKTD 162

RESULT 8
 A87544
 hypothetical protein CC2378 [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
 C:Accession: A87544
 R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 P., J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: A87544
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-324 <STO>
 A:Cross-references: GB:AE005673; NID:gl3423911; PIDN:AAK24349.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CC2378
 C:Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homolc

Query Match 55.3%; Score 42; DB 2; Length 324;
 Best Local Similarity 50.0%; Pred. No. 11;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGHQIYQFTDKD 13
 Db 244 GGHEVYINIGDND 255

RESULT 9
 T21106
 hypothetical protein F19B6.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T21106
 R:Thomas, K.
 submitted to the EMBL Data Library, February 1996
 A:Reference number: Z19375
 A:Accession: T21106
 A>Status: preliminary; translated from GB/EMBL/DBDB
 A:Molecule type: DNA
 A:Residues: 1-350 <WIL>
 A:Cross-references: EMBL:Z69635; NID:gl200023; PIDN:CAA93458.1; GSPDB:GN00022; CESP:F
 A:Experimental source: clone F19B6
 C:Genetics:
 A:Gene: CESP:F19B6.3
 A:Map position: 4
 A:Introns: 180/3; 274/2

Query Match 55.3%; Score 42; DB 2; Length 350;
 Best Local Similarity 46.2%; Pred. No. 12;
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGGHQIYQFTDKD 13
 Db 20 YNGRKIFDFTERD 32

RESULT 10
 T09378
 hypothetical protein F23K16.250 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 01-Dec-2000
 C:Accession: T09378; T04999
 R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.
 submitted to the Protein Sequence Database, June 1999
 A:Reference number: Z16652
 A:Accession: T09378
 A:Molecule type: DNA
 A:Residues: 1-563 <BEV>
 A:Cross-references: EMBL:AL078620; GSPDB:GN00062; ATSP:F23K16.250
 A:Experimental source: cultivar Columbia; BAC clone F23K16
 R:Bevan, M.; Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Hoheisel, J.; Mewes, H.W.
 submitted to the Protein Sequence Database, April 1998
 A:Reference number: Z15394
 A:Accession: T04999
 A:Molecule type: DNA
 A:Residues: 444-563 <BE2>
 A:Cross-references: EMBL:AL022605
 A:Experimental source: cultivar Columbia; BAC clone T19P19
 C:Genetics:
 A:Gene: ATSP:F23K16.250

A:Map position: 4
A:Introns: 118/3; 502/3
A:Note: T19P19.10

Query Match 55.3%; Score 42; DB 2; Length 563;
Best Local Similarity 58.3%; Pred. No. 21;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGHQIYQFTDKD 13
|||:| |||
Db 491 GGNQLTEFQDKD 502

RESULT 11

C86705
hypothetical protein yggA [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: C86705

R;Bolotin, A.; Wincker, P.; Manger, S.; Jaillon, O.; Malarre, K.; Weissbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: C86705

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-185 <STO>

A:Cross-references: GB:AE005176; PID:g12723547; PIDN:AAK04741.1; GSPDB:GN00146
A:Experimental source: strain IL1403

C:Genetics:

A:Gene: yggA

Query Match 53.9%; Score 41; DB 2; Length 185;
Best Local Similarity 53.6%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GHQIYQFTDKD 13
||| ||| |
Db 154 GHDFYVFTDAD 164

RESULT 12

T21690

hypothetical protein F33A8.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000

C:Accession: T21690

R;Matthews, L.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19459

A:Accession: T21690

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-467 <WIL>

A:Cross-references: EMBL:Z81525; PIDN:CA804258.1; GSPDB:GN00020; CESP:F33A8.4

A:Experimental source: clone F33A8

C:Genetics:

A:Gene: CESP:F33A8.4

A:Map position: 2

A:Introns: 29/3; 159/2; 212/3; 243/3; 266/3; 365/3

C:Superfamily: Caenorhabditis elegans hypothetical protein F33A8.4

Query Match 53.9%; Score 41; DB 2; Length 467;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGHHQIYQFTDK 12
| |||:| | :|
Db 368 YEGHKLYQHSEK 379

RESULT 13

D89775

hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: D89775

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
ma, A.; Mizutani-Ti, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: D89775

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-514 <KUR>

A:Cross-references: GB:BA000018; PID:g13700060; PIDN:BA841359.1; GSPDB:GN00149

A:Experimental source: strain N315

C:Genetics:

A:Gene: SA0139

Query Match 53.9%; Score 41; DB 2; Length 514;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGHQIYQFTDKD 13
||| ||| |
Db 449 GGRQIGQFSSKD 460

RESULT 14

G83445

conserved hypothetical protein PA1607 [imported] - Pseudomonas aeruginosa (strain PAO
C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: G83445

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L
.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: G83445

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-146 <STO>

A:Cross-references: GB:AE004588; GB:AE004091; MID:g9947563; PIDN:AAG04996.1; GSPDB:GN

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA1607

Query Match 52.6%; Score 40; DB 2; Length 146;
Best Local Similarity 63.6%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGHQIYQFTDK 12
| |||:| | :|
Db 75 GSHQYRLTDK 85

RESULT 15

H71979

probable type II restriction enzyme - Helicobacter pylori (strain J99)

C:Species: Helicobacter pylori

A:Variety: strain J99

C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 08-Oct-1999

C:Accession: H71979

R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Dolg, P.C.; Smith, D.

lives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F

Nature 397, 176-180, 1999

A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric p

A:Reference number: A71800; MUID:99120557; PMID:9923682

A:Accession: H71979

A:Status: preliminary

A:Molecule type: DNA

A;Residues: 1-260 <ARN>
A;Cross-references: GB:AE001444; GB:AE001439; NID:g4154549; PIDN:AAD05628.1; PID:g4154549
A;Experimental source: strain J99
C;Genetics:
A;Gene: jhp0046

Query Match 52.6%; Score 40; DB 2; Length 260;
Best Local Similarity 63.6%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGGHQIYQFTD 11
Db 194 FGGHQAQFND 204

Search completed: October 14, 2003, 08:40:48
Job time : 10.3854 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 08:35:36 ; Search time 4.13636 Seconds
(without alignments)
147.798 Million cell updates/sec

Title: US-09-931-700-2

Perfect score: 76

Sequence: 1 YGGRQYQFTDKD 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	57	75.0	185	1 ADML HUMAN	P35318 homo sapien
2	57	75.0	185	1 ADML RAT	P43145 rattus norv
3	57	75.0	188	1 ADML_PIG	P33366 sus scrofa
4	52	68.4	188	1 ADML_BOVIN	O62827 bos taurus
5	52	68.4	188	1 ADML_CANFA	P77559 canis famil
6	51	67.1	184	1 ADML_MOUSE	P97297 mus musculu
7	45.5	59.9	980	1 SYN_DROME	O24546 drosophila
8	39	51.3	425	1 SYH_METH	O26346 methanobact
9	39	51.3	705	1 PCPE_FLAME	P27028 flavobacter
10	39	51.3	1356	1 ROM2_YEAST	P51862 saccharomyc
11	38	50.0	422	1 TRSU_PYRKO	P58502 pyrococcus
12	38	50.0	532	1 CDPK_DAUCA	P28582 daucus caro
13	38	50.0	1337	1 DEXT_STRDO	P39653 streptococc
14	37.5	49.3	569	1 AMY_STRVL	P22998 streptomyc
15	37	48.7	257	1 HIS6_VIBCH	O9ksv8 vibrio chol
16	37	48.7	302	1 SI7D_HUMAN	Q9h4f1 h alpha-n-a
17	37	48.7	360	1 SI7D_MOUSE	Q9r2b6 mus musculu
18	37	48.7	367	1 I205_MYCTU	O53656 mycobacteri
19	37	48.7	424	1 CBPT_THEVU	P29068 thermoactin
20	37	48.7	463	1 SAH8_CAUOR	Q9ab08 caulobacter
21	37	48.7	464	1 DNAA_TREPA	O83047 treponema p
22	37	48.7	628	1 SNX1_HUMAN	Q96rf0 homo sapien
23	37	48.7	632	1 ETFD_SCHPO	P87111 s probable
24	37	48.7	644	1 YNL5_YEAST	P53925 saccharomyc
25	37	48.7	663	1 GR1A_BACCE	O85467 bacillus ce
26	37	48.7	1059	1 Y379_HUMAN	O15084 homo sapien
27	37	48.7	1071	1 TRI_THEAC	P96086 thermoplas
28	36.5	48.0	566	1 AMY_STRGR	P30270 streptomyc
29	36.5	48.0	566	1 AMY_STRLM	P09794 streptomyc
30	36	47.4	102	1 VATE_DESSY	O06503 desulfuroco
31	36	47.4	158	1 YKFG_ECOLI	O47685 escherichia
32	36	47.4	160	1 YFJV_ECOLI	P52140 escherichia
33	36	47.4	306	1 UL31_HSV11	P10215 herpes simp

34 36 47.4 493 1 MUEL_OCEIH Q8c2e6 oceanobacil
35 36 47.4 606 1 ACEA_MYCLE P48831 mycobacteri
36 36 47.4 608 1 GLMS_SAUTI Q8z2q2 s glucosami
37 36 47.4 640 1 RAEP_CANAL O93831 candida alb
38 36 47.4 1557 1 OSP_DROME Q27421 drosophila
39 35.5 46.7 281 1 Y149_MYGE P47395 mycoplasma
40 35 46.1 136 1 PSBR_TORAC Q40519 nicotiana t
41 35 46.1 138 1 PSBR_HORVU Q40070 hordeum vul
42 35 46.1 140 1 PSBR_SPIOL P10690 spinacia ol
43 35 46.1 209 1 CBFA_PETMA P10690 spinacia ol
44 35 46.1 222 1 THIE_BAGSU P39594 bacillus su
45 35 46.1 240 1 SPFA_SULSO Q97vp5 sulfolobus

ALIGNMENTS

RESULT 1
ADML_HUMAN
ID ADML_HUMAN STANDARD; PRT; 185 AA.
AC P35318;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)]
GN ADM OR AM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pherochromocytoma;
RX MEDLINE=93343928; PubMed=7688224;
RA Kitamura K., Sakata J., Kangawa K., Kojima M., Matsuo H., Eto T.;
RT "Cloning and characterization of cDNA encoding a precursor for human
adrenomedullin."
RL Biochem. Biophys. Res. Commun. 194:720-725(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94354869; PubMed=8074714;
RA Ishimitsu T., Kojima M., Kangawa K., Hino J., Matsuo H.,
RT Kitamura K., Eto T., Matsuo H.;
RL "Genomic structure of human adrenomedullin gene."
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Udell T.B., Toshyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rutterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT *Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 95-146.

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S -> R (in dbSNP:5005).
/FTID-VAR_014861.
SQ SEQUENCE 185 AA; 20420 MW; 64C7D2A0B4654DFE CRC64;
Query Match 75.0%; Score 57; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.0068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
Db 122 HQIYQFTDKD 131

RESULT 2
ADML RAT STANDARD; PRT; 185 AA.
ID ADML_RAT
AC P43145;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
DE terminal peptide (PROAM-N20) (PROAM N-terminal 20 peptide) (PAMP)].
DE ADM.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Sprague-Dawley; TISSUE=Adrenal gland;
RX MEDLINE=93384621; PubMed=7690563;
RA Sakata J., Shimokuba T., Kitamura K., Nakamura S., Kangawa K.,
RA Matsuo H., Eto T.;
RA "Molecular cloning and biological activities of rat adrenomedullin, a
RA hypotensive peptide.";
RA Biochem. Biophys. Res. Commun. 195:921-927(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=96102137; PubMed=8524787;
RX Wang X., Yue T.L., Barone F.C., White R.F., Clark R.K., Willette R.N.,
RX Sulpizio A.C., Aiyar N.V., Ruffolo R.R. Jr., Feuerstein G.Z.;
RX "Discovery of adrenomedullin in rat ischemic cortex and evidence for
RX its role in exacerbating focal brain ischemic damage.";
RX Proc. Natl. Acad. Sci. U.S.A. 92:11480-11484(1995).
RX [-] FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR
RX AGENTS.
CC [-] SUBCELLULAR LOCATION: Secreted.
CC [-] TISSUE SPECIFICITY: EXPRESSED IN ADRENAL GLANDS, LUNG, KIDNEY,
CC HEART, SPLEEN, DUODENUM AND SUBMANDIBULAR GLANDS.
CC [-] SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
CC -----
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CC -----
CC EMBL; D15069; BAA03665.1; -.
CC EMBL; U15419; AAB60519.1; -.
CC PIR; JN0766; JN0766.
CC InterPro; IPR001710; Adrenomedullin.
CC Pfam; PF02039; Adrenomedullin; 1.
CC PRINTS; PR00801; Adrenomedullin.
CC Hormone; Amidation; Cleavage on pair of basic residues; Signal.
CC SIGNAL 1 21
CC PROPEP 22 41
CC PROPEP 45 91
CC PEPTIDE 94 143
CC PROPEP 149 185
CC PREPROAM C-TERMINAL FRAGMENT (BY
CC SIMILARITY).

```

FT DISULFID 107 112 BY SIMILARITY.
 FT MOD_RES 41 41 AMIDATION (G-42 PROVIDE AMIDE GROUP)
 FT (BY SIMILARITY).
 FT MOD_RES 143 143 AMIDATION (G-144 PROVIDE AMIDE GROUP)
 FT (BY SIMILARITY).
 SQ SEQUENCE 185 AA; 20636 MW; 35CAD9A9DD19AE35 CRC64;
 Query Match 75.0%; Score 57; DB 1; Length 185;
 Best Local Similarity 100.0%; Pred. No. 0.0068;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQIYQFTDKD 13
 |||||
 Db 119 HQIYQFTDKD 128

RESULT 3
 ADML_PIG STANDARD; PRT; 188 AA.
 AC P53366;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
 DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
 GN ADM OR AM.
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Adrenal medulla;
 RX MEDLINE=94139945; PubMed=8043068;
 RA Kitamura K., Kangawa K., Kojima M., Ichiki Y., Matsuo H., Eto T.;
 RA Kawamoto M., Minamino N., Matsuo H., Eto T.;
 RT "Identification and hypotensive activity of proadrenomedullin
 RT N-terminal 20 peptide (PAMP).";
 RL FEBS Lett. 351:35-37(1994).
 CC -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR
 CC AGENTS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ADRENAL GLANDS, LUNG, AND
 CC KIDNEY.
 CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
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 CC -----
 DR EMBL; D14875; BAA03590.1; -
 DR PIR; S41600; S41600.
 DR InterPro; IPR001710; Adrenomedullin.
 DR Pfam; PF02039; Adrenomedullin; 1.
 DR PRINTS; PR00801; ADRENOMEDULLIN.
 KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.
 FT SIGNAL 1 21
 FT PROPEP 22 41 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
 FT PROPEP 45 92
 FT PEPTIDE 95 146
 FT PROPEP 153 188
 FT PREPROAM C-TERMINAL FRAGMENT (BY

FT DISULFID 110 115 BY SIMILARITY.
 FT MOD_RES 41 41 AMIDATION (G-42 PROVIDE AMIDE GROUP).
 FT MOD_RES 146 146 AMIDATION (G-147 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 188 AA; 20893 MW; 71749460F5660A61 CRC64;
 Query Match 75.0%; Score 57; DB 1; Length 188;
 Best Local Similarity 100.0%; Pred. No. 0.0069;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 HQIYQFTDKD 13
 |||||
 Db 122 HQIYQFTDKD 131

RESULT 4
 ADML_BOVIN STANDARD; PRT; 188 AA.
 AC O62827;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
 DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
 GN ADM.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Aorta;
 RX MEDLINE=98244567; PubMed=9585168;
 RA Baker S., Wood E., Clark A.J.L., Corder R.;
 RT "Cloning of bovine preadrenomedullin and inhibition of its basal
 RT expression in vascular endothelial cells by staurosporine.";
 RL Life Sci. 62:1407-1415(1998).
 CC -1- FUNCTION: HYPOTENSIVE PEPTIDE. MAY FUNCTION AS A HORMONE IN
 CC CIRCULATION CONTROL (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
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 CC -----
 DR EMBL; AJ001613; CAA04866.1; -
 DR InterPro; IPR001710; Adrenomedullin.
 DR Pfam; PF02039; Adrenomedullin; 1.
 DR PRINTS; PR00801; ADRENOMEDULLIN.
 KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.
 FT SIGNAL 1 21
 FT PROPEP 22 41 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
 FT PROPEP 45 92
 FT PEPTIDE 95 146
 FT PROPEP 148 188
 FT PREPROAM C-TERMINAL FRAGMENT (BY
 FT SIMILARITY).
 FT DISULFID 110 115
 FT MOD_RES 41 41
 FT AMIDATION (G-42 PROVIDE AMIDE GROUP)
 FT (BY SIMILARITY).
 FT MOD_RES 146 146
 FT AMIDATION (G-147 PROVIDE AMIDE GROUP)
 FT (BY SIMILARITY).
 SQ SEQUENCE 188 AA; 20981 MW; 3002E79AB3B6612C CRC64;
 Query Match 68.4%; Score 52; DB 1; Length 188;
 Best Local Similarity 90.0%; Pred. No. 0.052;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
 Db 122 HQIYHFTDKD 131

RESULT 5

ADML_CANFA STANDARD; PRT; 188 AA.
 AC O7759; Q9TWC9;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
 DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
 GN ADM.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Imoto I., Jougasaki M.;
 RT "Cloning of cDNA encoding canine adrenomedullin.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99002704; PubMed=9788655;
 RX Ono Y., Kojima M., Okada K., Kangawa K.;
 RT "cDNA cloning of canine adrenomedullin and its gene expression in the
 RT heart and blood vessels in endotoxin shock.";
 RL Shock 10:243-247(1998).
 CC -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR
 CC AGENTS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.

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 CC -----

EMBL; AF045773; AAD05423.1; -
 DR EMBL; U96127; RAD09957.1; -
 DR InterPro: IPR001710; Adrenomedullin.
 DR Pfam; PF02039; Adrenomedullin; 1.
 DR PRINTS; PR00801; Adrenomedullin.
 KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT PEPTIDE 22 41 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
 FT PROPEP 45 92 BY SIMILARITY.
 FT PEPTIDE 95 146 ADRENOMEDULLIN.
 FT PROPEP 148 188 ADRENOMEDULLIN.
 FT BY SIMILARITY.
 FT FT BY SIMILARITY.
 FT MOD_RES 110 115 AMIDATION (G-42 PROVIDE AMIDE GROUP)
 FT (BY SIMILARITY).
 FT MOD_RES 146 146 AMIDATION (G-147 PROVIDE AMIDE GROUP)
 FT (BY SIMILARITY).
 FT CONFLICT 130 130 N -> K (IN REF. 2).
 FT SEQUENCE 188 AA; 20929 MW; 809D6A64F98F5578 CRC64;

Query Match 58.4%; Score 52; DB 1; Length 188;
 Best Local Similarity 90.0%; Pred. No. 0.052;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
 Db 122 HQIYQFTDND 131

RESULT 6

ADML_MOUSE STANDARD; PRT; 184 AA.
 AC P97297; P97453;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
 DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
 GN ADM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=129/Sv;
 RX MEDLINE=97092892; PubMed=8938454;
 RA Okazaki T., Ogawa Y., Tamura N., Mori Y., Isse N., Aoki T.,
 RA Rochelle J.M., Taketo M.M., Seldin M.F., Nakao K.;
 RT "Genomic organization, expression, and chromosomal mapping of the
 RT mouse adrenomedullin gene.";
 RL Genomics 37:395-399(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6J;
 RX MEDLINE=99046755; PubMed=9808778;
 RA Yotsumoto S., Shimada T., Cui C.Y., Nakashima H., Fujiwara H.,
 RA Ko M.S.H.;
 RT "Expression of adrenomedullin, a hypotensive peptide, in the
 RT trophoblast giant cells at the embryo implantation site in mouse.";
 RL Dev. Biol. 203:264-275(1998).
 CC -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR
 CC AGENTS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.

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 CC -----

EMBL; D78349; EAA11367.1; -
 DR EMBL; U77630; AAB36535.1; -
 DR MGD; MGI:108058; Agm.
 DR InterPro: IPR001710; Adrenomedullin.
 DR Pfam; PF02039; Adrenomedullin; 1.
 DR PRINTS; PR00801; Adrenomedullin.
 KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT PEPTIDE 22 41 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
 FT PROPEP 45 92 BY SIMILARITY.
 FT PEPTIDE 95 144 ADRENOMEDULLIN.
 FT PROPEP 151 184 ADRENOMEDULLIN.
 FT BY SIMILARITY.
 FT DISULFID 108 113 AMIDATION (G-42 PROVIDE AMIDE GROUP)
 FT (BY SIMILARITY).
 FT MOD_RES 144 144 AMIDATION (G-145 PROVIDE AMIDE GROUP)
 FT (BY SIMILARITY).
 FT CONFLICT 173 173 A -> G (IN REF. 2).
 FT SEQUENCE 184 AA; 20764 MW; C88C99045A79C898 CRC64;

Query Match 67.1%; Score 51; DB 1; Length 184;
 Best Local Similarity 90.0%; Pred. No. 0.076;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13
 Db 120 HQIYQLTDKD 129

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RESULT 7
SYN_DROME
ID SYN_DROME STANDARD; PRT; 980 AA.
AC Q24546; Q24545;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Synapsin.
GN SYN OR SYN1.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS SYN-S AND SYN1-RT).
RC STRAIN=Berlin; TISSUE=Head;
RX MEDLINE=96209149; PubMed=8627354;
RA Klages B.R.E., Heimbeck G., Godenschwege T.A., Hofbauer A.,
RA Pflugfelder G.O., Reifegerste R., Reisch D., Schaupp M., Buchner S.,
RA Buchner E.
RT "Invertebrate synapsins: a single gene codes for several isoforms in
Drosophila."
RL J. Neurosci. 16:3154-3165(1996).
CC -!- SUBCELLULAR LOCATION: SYNAPSE.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name-Syn1-RT;
CC isoId=Q24546-1; Sequence=Displayed;
CC Name-Syn-S;
CC isoId=Q24546-2; Sequence=VSP_006324;
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN THE NERVOUS SYSTEM.
CC -!- SIMILARITY: BELONGS TO THE SYNAPSIN FAMILY.
CC -----
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CC -----
DR EMBL; X95453; CAA64723.1; -
DR EMBL; X95453; CAA64722.1; -
DR HSSP; P17599; 1AUX.
DR FlyBase; FBgn0004575; Syn.
DR InterPro; IPR001359; Synapsin.
DR Pfam; PF02078; Synapsin; 1.
DR Pfam; PF02750; Synapsin; 1.
DR PRINTS; PR01368; SYNAPSIN.
DR PROSITE; PS00415; SYNAPSIN_1; FALSE NEG.
DR PROSITE; PS00416; SYNAPSIN_2; FALSE NEG.
DR Synapse; Neurone; Alternative splicing.
KW Synapsin
FT DOMAIN 2 7
FT DOMAIN 668 680 POLY-PRO.
FT DOMAIN 692 695 POLY-SER.
FT DOMAIN 698 703 POLY-PRO.
FT VARSPLIC 539 980 Missing (in isoform Syn-S).
FT FTId=VSP_006324.
SQ SEQUENCE 980 AA; 102799 MW; E6037A2A4604F944 CRC64;

Query Match 59.9%; Score 45.5; DB 1; Length 980;
Best Local Similarity 52.6%; Pred. No. 4;
Matches 10; Conservative 0; Mismatches 2; Indels 7; Gaps 1;

QY 1 YGG-----HQIYQFTDK 12
||| |
Db 181 YGGVPSINSLSHYQFDK 199

RESULT 8
SYN_METTH
ID SYN_METTH STANDARD; PRT; 425 AA.
AC Q26346;
DT 15-JUL-1998 (Rel. 36, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
DE (HISRS).
GN HISS OR MTH244.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Hashizadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwni N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shiner G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics."
RL J. Bacteriol. 179:7135-7155(1997).
CC -!- CATALYTIC ACTIVITY: ATP + L-histidine + tRNA(His) -> AMP +
CC diphosphate + L-histidyl-tRNA(His).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
CC -----
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CC -----
DR EMBL; AE000811; AAB84750.1; ALT_INIT.
DR HSSP; O32422; IQE0.
DR HAMAP; MF_00127; -; 1.
DR InterPro; IPR004154; HGTP-anticodon.
DR InterPro; IPR004516; HISS.
DR InterPro; IPR002314; tRNA-synt_2b.
DR InterPro; IPR006195; tRNA_ligase_II.
DR Pfam; PF03129; HGTP-anticodon; 1.
DR Pfam; PF00587; tRNA-synt_2b; 1.
DR TIGRFAMS; TIGR00442; hisS; 1.
DR PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
SQ SEQUENCE 425 AA; 48019 MW; 8388A5975A017535 CRC64;

Query Match 51.3%; Score 39; DB 1; Length 425;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 HQIYQFTDK 12
:|||||
Db 60 NQIYHFTDK 68

RESULT 9
PPCE_FLAME
ID PPCE_FLAME STANDARD; PRT; 705 AA.
AC P27028;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Prolyl endopeptidase precursor (EC 3.4.21.26) (Proline-specific
DE endopeptidase) (PSE) (post-proline cleaving enzyme) (PE).

```

GN FlPEP1.
OS Flavobacterium meningosepticum (Chryseobacterium meningosepticum).
OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
OC Flavobacteriaceae; Chryseobacterium.
OX NCBI_TaxID=238;
RN [1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=92176159; PubMed=1840588;
RA Yoshimoto T., Kanatani A., Shinoda T., Inaoka T., Kokubo T., Tsuru D.;
RT "Prolyl endopeptidase from Flavobacterium meningosepticum: cloning
RT and sequencing of the enzyme gene.";
RT J. Biochem. 110:873-878(1991).
RN [2]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=94114173; PubMed=7764331;
RA Dieftenthal T., Dargatz H., Witte V., Reipen G., Svendsen I.;
RT "Cloning of proline-specific endopeptidase gene from Flavobacterium
RT meningosepticum: expression in Escherichia coli and purification of
RT the heterologous protein.";
RL Appl. Microbiol. Biotechnol. 40:90-97(1993).
CC -!- FUNCTION: CLEAVES PEPTIDE BONDS ON THE C-TERMINAL SIDE OF PROLYL
CC RESIDUES WITHIN PEPTIDES THAT ARE UP TO APPROXIMATELY 30 AMINO
CC ACIDS LONG. HAS AN ABSOLUTE REQUIREMENT FOR AN X-PRO BOND IN THE
CC TRANS CONFIGURATION IMMEDIATELY PRECEDING THE PRO-Y SCISSIBLE
CC BOND.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of Pro-|-Xaa >> Ala-|-Xaa in
CC oligopeptides.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Periplasmic.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9A.
CC
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CC
CC EMBL; D10980; BAA01755.1; -.
CC EMBL; X63674; CA445213.1; -.
CC PIR; JX0194; JX0194.
CC HSP; P23687; IQFM.
CC MEROPS; S09.001; -.
CC InterPro; IPR001375; Peptidase_S9.
CC InterPro; IPR004106; Peptidase_S9_N.
CC InterPro; IPR002471; ProL_endopep_ser.
CC InterPro; IPR002470; Proligo_Ptase.
CC InterPro; IPR000379; Ser_estrs_site.
CC Pfam; PF00326; Peptidase_S9; 1.
CC Pfam; PF02897; Peptidase_S9_N; 1.
CC PRINTS; PR00852; PROLIGOPTASE.
CC DR PROSITE; PS00708; PRO-ENDOPEP_SER; 1.
KW Hydrolase; Serine protease; Periplasmic; Signal.
FT SIGNAL 1 20
FT CHAIN 21 705 PROLYL ENDOPEPTIDASE.
FT ACT_SITE 556 556 CHARGE RELAY SYSTEM.
FT ACT_SITE 675 675 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CONFLICT 110 110 S -> C (IN REF. 2).
FT CONFLICT 587 587 R -> A (IN REF. 2).
SQ SEQUENCE 705 AA; 78707 MW; BCUEDCBAB328256 CRC64;
Query Match 51.3%; Score 39; DB 1; Length 705;
Best Local Similarity 63.6%; Pred. No. 39;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 3 GHQIYQFTDKD 13
| : | | | | |
Db 306 GGTLYLFTDKD 316
RESULT 10
ROM2_YEAST

ID ROM2_YEAST STANDARD; PRT; 1356 AA.
AC P51862;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE RH01 GDP-GTP exchange protein 2.
GN ROM2 OR YLR371W OR L8039.3.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RN SEQUENCE FROM N.A.
RX STRAIN=S288c / AB972;
RX MEDLINE=97313267; PubMed=9169871;
RA Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansoerge W.,
RA Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A.,
RA Entian K.-D., Floeth M., Goifeau A., Hebling U., Heumann K.,
RA Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P.,
RA Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,
RA Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M.,
RA Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M.,
RA Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S.,
RA Underwood A.P., Urrestazu L.A., Vandenbol M., Verhasselt P.,
RA Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,
RA Wedler H., Zimmermann F.K., Zollner A., Hani J., Hohelsel J.D.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
RL Nature 387:87-90(1997).
RN [2]
RN CHARACTERIZATION.
RX MEDLINE=96208506; PubMed=8641285;
RA Ozaki K., Tanaka K., Imamura H., Hihara T., Kameyama T.,
RA Nonaka H., Hirano H., Matsuura Y., Takai Y.;
RT "Rom1p and Rom2p are GDP/GTP exchange proteins (GEPs) for the Rhopl
RT small GTP binding protein in Saccharomyces cerevisiae.";
RL EMBO J. 15:2196-2207(1996).
CC -!- FUNCTION: STIMULATES THE EXCHANGE OF RH01 GDP-BOUND FORM INTO
CC GTP-BOUND FORM.
CC
CC -!- SIMILARITY: Contains 1 DBL-homology (DH) domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U19103; AAB67564.1; -.
CC PIR; S51389; S51389.
CC SGD; S0004363; ROM2.
CC GO; GO:0005934; C:bud tip; IDA.
CC GO; GO:0005089; F:rho guanyl-nucleotide exchange factor activity; IDA.
CC GO; GO:0004871; F:signal transducer activity; IPI.
CC GO; GO:0007117; P:bud growth; IPI.
CC GO; GO:0007047; P:cell wall organization and biogenesis; IPI.
CC GO; GO:0000283; P:establishment of cell polarity (sensu Sacch.); IPI.
CC GO; GO:0007264; P:small GTPase mediated signal transduction; IPI.
CC InterPro; IPR001180; Citron.
CC InterPro; IPR000591; DEP.
CC InterPro; IPR001331; GDS_CDC24.
CC InterPro; IPR000219; RhoGEF.
CC Pfam; PF00780; CNH; 1.
CC Pfam; PF00610; DEP; 1.
CC Pfam; PF00621; RhoGEF; 1.
CC SMART; SM00036; CNH; 1.
CC SMART; SM00049; DEP; 1.
CC SMART; SM00325; RhoGEF; 1.
CC PROSITE; PS00741; DH_1; FALSE_NEG.
CC PROSITE; PS00101; DH_2; 1.
KW Guanine-nucleotide releasing factor.
FT DOMAIN 659 846 DH.
FT DOMAIN 252 265 POLY-ASN.

```

FT DOMAIN 329 336 POLY-HIS.
FT DOMAIN 632 635 POLY-ASP.
SQ SEQUENCE 1356 AA; 152595 MW; 5FBC542114E7BC92 CRC64;

Query Match
Best Local Similarity 51.3%; Score 39; DB 1; Length 1356;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 HOIQYFTD 11
Db 496 HEVYEFTD 503

RESULT 11
TKSU_PYRKO STANDARD; PRT; 422 AA.
AC P58502; Q977F5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE TK-subtilisin precursor (EC 3.4.21.-).
OS Pyrococcus kodakaraensis.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Thermococcus.
OX NCBI_TaxID=69014;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN-KOD1;
RX MEDLINE-21266834; PubMed-11375149;
RA Kannan Y., Koga Y., Inoue Y., Haruki M., Takagi M., Imanaka T.,
RA Morikawa M., Kanaya S.;
RT "Active subtilisin-like protease from a hyperthermophilic archaeon in
a form with a putative prosequence.";
RL Appl. Environ. Microbiol. 67:2445-2452(2001).
CC -1- FUNCTION: Has a broad substrate specificity with a slight
preference to large hydrophobic amino acid residues at the P1
position.
CC -1- COFACTOR: Calcium.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MISCELLANEOUS: Thermostable; high activity at 80 degrees Celsius.
CC -1- OPTIMAL pH is 9.5.
CC -1- SIMILARITY: Belongs to peptidase family S8.

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EMBL; AB056701; BAB60701.1;
DR InterPro; IPR000209; Peptidase_S8.
DR Pfam; PF00082; Peptidase_S8; 1.
DR PRINTS; PR00723; SUBTILISIN.
DR PROSITE; PS00136; SUBTILASE ASP; 1.
DR PROSITE; PS00138; SUBTILASE SER; 1.
KW Hydrolase; Serine protease; Calcium-binding; Zymogen; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT PROPEP 25 106
FT CHAIN 107 422 TK-SUBTILISIN.
FT ACT_SITE 139 139 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 177 177 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 348 348 CHARGE RELAY SYSTEM (BY SIMILARITY).
SQ SEQUENCE 422 AA; 43785 MW; 843255BCD806DB71 CRC64;

Query Match
Best Local Similarity 50.0%; Score 38; DB 1; Length 422;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGHQYQF 9
Db 50 GGHVYQF 57

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```

Db 50 GGHVYQF 57

RESULT 12
CDPK_DAUCA STANDARD; PRT; 532 AA.
AC P28582;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcium-dependent protein kinase (EC 2.7.1.-) (CDPK).
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridaceae; campanulids; Apiales; Apiaceae; Daucus.
OX NCBI_TaxID=4039;
RN [1]
RP SEQUENCE FROM N.A.
RA Choi J.H.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RX MEDLINE-92003674; PubMed-1912486;
RA Suen K.-L., Choi J.H.;
RT "Isolation and sequence analysis of a cDNA clone for a carrot
calcium-dependent protein kinase: homology to
calcium/calmodulin-dependent protein kinases and to calmodulin.";
RL Plant Mol. Biol. 17:581-590(1991).
CC -1- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
INVOLVE CALCIUM AS A SECOND MESSENGER.
CC -1- ENZYME REGULATION: ACTIVATED BY CALCIUM. AUTOPHOSPHORYLATION MAY
PLAY AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CAMK SUBFAMILY.
CC -1- SIMILARITY: Contains 4 EF-hand calcium-binding domains.

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EMBL; X56599; CAA39936.1;
DR PIR; S17759; S17759.
DR PIR; T14335; T14335.
DR HSSP; Q63450; 1A06.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00018; EF_HAND; 4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR TRANSFERASE; Serine/threonine-protein kinase; ATP-binding;
Calcium-binding; Phosphorylation.
FT DOMAIN 81 339 PROTEIN KINASE.
FT BINDING 87 95 ATP (BY SIMILARITY).
FT BINDING 110 110 ATP (BY SIMILARITY).
FT ACT_SITE 205 205 BY SIMILARITY.
FT CA_BIND 395 406 EF-HAND 1 (POTENTIAL).
FT CA_BIND 431 442 EF-HAND 2 (POTENTIAL).
FT CA_BIND 465 476 EF-HAND 3 (POTENTIAL).
FT CA_BIND 500 511 EF-HAND 4 (POTENTIAL).
SQ SEQUENCE 532 AA; 60065 MW; F03E6F036A0AE348 CRC64;

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Query Match 50.0%; Score 38; DB 1; Length 532;
 Best Local Similarity 60.0%; Pred. No. 44;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 HOIYQFTDKD 13
 ||:|:|:|
 DB 458 HQAFYFDKD 467

RESULT 13

DEXT_STRDO STANDARD; PRT: 1337 AA.
 AC P3953;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Dextranase precursor (EC 3.2.1.11) (Alpha-1,6-glucan-6-glucanohydrolase).
 DE DEX.
 GN DEX.
 OS Streptococcus downei (Streptococcus sobrinus).
 OG Plasmid pYA902.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1317;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-36.
 RC STRAIN=6715 / UAB66;
 RX MEDLINE=94292401; PubMed=8021165;
 RA Wanda S.-Y., Curtiss R. III;
 RT "Purification and characterization of Streptococcus sobrinus dextranase produced in recombinant Escherichia coli and sequence analysis of the dextranase gene."
 RT J. Bacteriol. 176:3839-3850(1994).
 RL -!- FUNCTION: MAY PLAY A ROLE IN SUCROSE-INDEPENDENT ADHERENCE TO THE PELLICULE-COATED TOOTH SURFACE.
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,6-alpha-D-glucosidic linkages in dextran.
 CC -!- SUBUNIT: Homodimer.
 CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (Potential).
 CC -!- MISCELLANEOUS: The activity of this enzyme is optimal at pH 5.3 and at 39 degrees Celsius.
 CC -!- SIMILARITY: BELONGS TO FAMILY 66 OF GLYCOSYL HYDROLASES.
 CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-5 IS THE INITIATOR.
 CC
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 CC
 CC EMBL: M96978; AAA21772.1; .
 CC InterPro: IPR001899; Gram_pos_anchor.
 CC InterPro: IPR006192; LPXTG.
 CC Pfam: PF00746; Gram_pos_anchor; 1.
 CC TIGRPFAMS: TIGR01167; LPXTG_anchor; 1.
 CC PROSITE: P50847; GRAM_POS_ANCHORING; 1.
 KW Hydrolase; Glycosidase; Cell wall; Peptidoglycan-anchor; Repeat;
 KW Signal; Plasmid.
 FT SIGNAL 1 30
 FT CHAIN 31 1308 DEXTRANASE.
 FT PROPEP 1309 1337 REMOVED BY SORTASE (POTENTIAL).
 FT SITE 1305 1309 LPXTG SORTING SIGNAL (POTENTIAL).
 FT MOD_RES 1308 1308 AMIDE-LINKED TO CELL WALL (POTENTIAL).
 SQ SEQUENCE 1337 AA; 143298 MW; B494275A7A2E3D0 CRC64;

Query Match 50.0%; Score 38; DB 1; Length 1337;
 Best Local Similarity 41.7%; Pred. No. 11e+02;
 Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGHQIYQFTDKD 13

DB 457 GDNEVSYADKD 468

RESULT 14

AMY_STRVL STANDARD; PRT: 569 AA.
 AC P22998;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
 DE AML.
 GN AML.
 OS Streptomyces violaceus (Streptomyces venezuelae).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1936;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15068;
 RX MEDLINE=89232724; PubMed=3266752;
 RA Virolle M.-J., Long C.M., Chang S., Bibb M.J.;
 RT "Cloning, characterization and regulation of an alpha-amylase gene from Streptomyces venezuelae."
 RL Gene 74:321-334(1988).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.
 CC -!- INDUCTION: BY MALTOSE, AND REPRESSION BY GLUCOSE.
 CC -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC
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 CC
 CC EMBL: M25263; AAB36561.1; .
 CC PIR: JS0101; JS0101.
 CC HSP: P29957; IAQM.
 CC InterPro: IPR006589; Alp_amyl_cat_sub.
 CC InterPro: IPR006048; Alpha_amyl_C.
 CC InterPro: IPR006047; Alpha_amyl_cat.
 CC InterPro: IPR002044; CBD_4.
 CC InterPro: IPR006046; Glyco_hydro_13.
 CC Pfam: PF00128; alpha-amylase; 1.
 CC Pfam: PF02806; alpha-amylase_C; 1.
 CC Pfam: PF00686; CBM_20; 1.
 CC PRINTS: PR00110; ALPHAAMYLASE.
 CC PRODOM: PD001568; CBD_4; 1.
 CC SMART: SM00642; Amy; 1.
 CC SMART: SM00632; Amy_C; 1.
 KW Hydrolase; Glycosidase; Carbohydrate metabolism; Signal.
 FT SIGNAL 1 28 POTENTIAL.
 FT CHAIN 29 569 ALPHA-AMYLASE.
 FT ACT_SITE 205 205 BY SIMILARITY.
 FT ACT_SITE 209 209 BY SIMILARITY.
 FT ACT_SITE 296 296 BY SIMILARITY.
 SQ SEQUENCE 569 AA; 60637 MW; 14CA5BD56720043 CRC64;

Query Match 49.3%; Score 37.5; DB 1; Length 569;
 Best Local Similarity 50.0%; Pred. No. 58;
 Matches 8; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

QY 1 YGG---HQIYQFTDKD 13
 ||:|:|:|
 DB 324 YGSPDVHSGYEWTDKD 339

RESULT 15

Job time : 7.13636 secs

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HIS6_VIBCH
ID HIS6_VIBCH STANDARD; PRT; 257 AA.
AC C9KSW8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Imidazole glycerol phosphate synthase subunit hisF (EC 4.1.3.-) (IGP
DE synthase cyclase subunit) (IGP synthase subunit hisF) (ImGP synthase
DE subunit hisF) (IGPS subunit hisF).
GN HISF OR VC1138.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=E1 Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unwayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Niernan W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RL Nature 406:477-483 (2000).
CC -!- FUNCTION: IGPS catalyzes the conversion of PRFAR and glutamine to
CC IGP, AICAR and glutamate. The hisF subunit catalyzes the
CC cyclization activity that produces IGP and AICAR from PRFAR using
CC the ammonia provided by the hisH subunit (By similarity).
CC -!- CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyribulos-1-
CC ylaminomethylideneamino)-1-(5'-phosphoribosyl)]imidazole-4'-
CC carboxamide + L-glutamine -> imidazole-glycerol phosphate + 5-
CC aminoimidazol-4-carboxamide ribonucleotide + L-glutamate + H(2)O.
CC -!- PATHWAY: Histidine biosynthesis; fifth step.
CC -!- SUBUNIT: Heterodimer of hisH and hisF (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE HISA / HISF FAMILY.
CC -----
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CC -----
CC EMBL; AE004193; AAF94297.1; -.
CC PIR; E82238; E82238.
CC TIGR; VC1138; -.
CC HAMAP; MF_01013; -.
CC InterPro; IPR003009; FMN_enzyme.
CC InterPro; IPR006062; His_biosynth.
CC InterPro; IPR004651; HisF.
CC Pfam; PF00977; His_biosynth; 1.
CC TIGRFAMs; TIGR00735; hisF; 1.
KW Histidine biosynthesis; lyase; Complete proteome.
FT ACT_SITE 11 11 POTENTIAL.
FT ACT_SITE 130 130 POTENTIAL.
SQ SEQUENCE 257 AA; 28338 MW; F722BBCA3BEB153C CRC64;

Query Match 48.7%; Score 37; DB 1; Length 257;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGHQYQFT 10
Db 138 GQYQYQFT 146

```

Search completed: October 14, 2003, 08:39:09

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 08:36:06 ; Search time 17.4318 Seconds
(without alignments)
192.446 Million cell updates/sec

Title: US-09-931-700-2

Perfect score: 76

Sequence: 1 YGGHQIYQFTDKD 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mmc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	57	75.0	27	6	Q9TRZ6
2	52	68.4	188	6	Q95KP0
3	51	67.1	643	16	Q55549
4	45.5	59.9	348	5	Q81NM4
5	45.5	59.9	388	5	Q24544
6	45.5	59.9	443	5	Q9VH15
7	45.5	59.9	537	5	Q81NM6
8	45	59.2	776	10	Q81050
9	44	57.9	514	2	Q9XSR9
10	44	57.9	2231	16	Q9ZKK7
11	42	55.3	173	5	Q8MXJ0
12	42	55.3	184	16	Q9EWO4
13	42	55.3	280	16	Q45612
14	42	55.3	324	16	Q9A5R9
15	42	55.3	326	16	Q8RCV8
16	42	55.3	350	5	Q19582

17	42	55.3	563	10	Q9SV96
18	42	55.3	1206	3	Q9UT2
19	41	53.9	185	2	Q9L474
20	41	53.9	185	16	Q9CHS8
21	41	53.9	467	5	Q62214
22	41	53.9	514	16	Q9XK71
23	41	53.9	514	16	Q8NVQ7
24	40.5	53.3	466	5	Q76322
25	40.5	53.3	503	5	Q76323
26	40	52.6	106	4	Q9UGX0
27	40	52.6	146	16	Q913B4
28	40	52.6	229	2	Q8VTE0
29	40	52.6	260	16	Q9ZN14
30	40	52.6	261	2	Q8VTB6
31	40	52.6	261	2	Q8VTE3
32	40	52.6	261	2	Q8VLL3
33	40	52.6	261	2	Q8VTE5
34	40	52.6	261	2	Q8VTE8
35	40	52.6	275	5	Q16622
36	40	52.6	340	5	Q96512
37	40	52.6	377	16	Q8KCL8
38	40	52.6	470	4	Q9BSU7
39	40	52.6	470	11	Q99LFO
40	40	52.6	687	10	Q8S011
41	40	52.6	769	10	Q943E0
42	40	52.6	1298	11	Q8CHG6
43	40	52.6	1841	4	Q15031
44	39.5	52.0	606	3	Q9USQ7
45	39	51.3	95	16	Q8EPG1

ALIGNMENTS

RESULT 1

Q9TRZ6	PRELIMINARY;	PRT;	27 AA.
ID	Q9TRZ6		
AC	Q9TRZ6;		
DT	01-MAY-2000 (TRENBLrel. 13, Created)		
DT	01-MAY-2000 (TRENBLrel. 13, Last sequence update)		
DT	01-JUN-2002 (TRENBLrel. 21, Last annotation update)		
DE	ADRENOMEDULLIN.		
OS	Sus scrofa (pig).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
OX	NCHI_TaxID=9823;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=96157714; PubMed=8576091;		
RA	Ichiki Y., Kitamura K., Kangawa K., Kawamoto M., Matsuo H., Eto T.;		
RT	"Distribution and characterization of immunoreactive adrenomedullin in porcine tissue, and isolation of adrenomedullin [26-52] and adrenomedullin [34-52] from porcine duodenum.";		
RL	J. Biochem. 118:765-770(1995).		
DR	InterPro; IPR001710; Adrenomedullin.		
DR	Pfam; PF02039; Adrenomedullin; 1.		
DR	PRINTS; PR08081; ADRENOMEDULLIN.		
SQ	SEQUENCE 27 AA; 3063 MW; B8DC7FA18B3D90 CRC64;		

Query Match 75.0%; Score 57; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HQIYQFTDKD 13

Db 3 HQIYQFTDKD 12

RESULT 2

Q95KP0	PRELIMINARY;	PRT;	188 AA.
ID	Q95KP0		
AC	Q95KP0;		
DT	01-DEC-2001 (TRENBLrel. 19, Created)		

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Adrenomedullin.
 GN PBAM-2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kitamura K., Matsui E., Kato J., Katoh F., Kita T., Tsuji T.,
 RA Kangawa K., Eto T.;
 RT "ADRENOMEDULLIN (11-26): AN ENDOGENOUS HYPERTENSIVE PEPTIDE ISOLATED
 RT FROM BOVINE ADRENAL MEDULLA.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB055107; BAB62176.1; -;
 DR InterPro: IPR001710; Adrenomedullin.
 DR Pfam: PF02039; Adrenomedullin; 1.
 DR PRINTS: PRO0801; ADRENOMEDULLIN.
 SQ SEQUENCE 188 AA; 20963 MW; 6102E69A756DCA86 CRC64;
 Query Match 68.4%; Score 52; DB 6; Length 188;
 Best Local Similarity 90.0%; Pred. No. 0.54;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 HQIYQFTDKD 13
 Db 122 HQIYHFTDKD 131
 RESULT 3
 Q5549
 ID Q5549 PRELIMINARY; PRT; 643 AA.
 AC Q5549;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein sir0168.
 GN SIR0168.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OX NCBI_TaxID=1148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCC 6803;
 RA Tabata S.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96127529; PubMed=8590279;
 RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
 RA Sugita M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
 RT region from map positions 64% to 92% of the genome.";
 RL DNA Res. 2:153-166(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hiroseawa M., Sugita M., Sasamoto S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
 RA Shimpō S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
 RA Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 DR EMBL: D33999; BAA10047.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 643 AA; 68369 MW; 1EE900ID3332B411 CRC64;

Query Match 67.1%; Score 51; DB 16; Length 643;
 Best Local Similarity 72.7%; Pred. No. 3;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3 GHQIYQFTDKD 13
 Db 447 GHEIYQYTDPD 457
 RESULT 4
 Q8INM4
 ID Q8INM4 PRELIMINARY; PRT; 348 AA.
 AC Q8INM4;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE CG3985-PC.
 GN SYN.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abell J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler J., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Hanzon J., An H., Balowin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 McIntosh T.C., Moy M., Murphy B., Nelson K.A., Nunoo J.,
 Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Scheeler F.,
 Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 Stapleton M., Strong R., Svirkas R., Tector C., Tyler D.,
 Williams S.M., Zaveri J.S., Smith H.O., Venter C.J., Rubin G.M.;
 "Sequencing of Drosophila melanogaster genome."
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [3]
 RN
 RP
 SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 Hradecky P., Huang Y., Kamnik J.S., Prochnik S.E., Smith C.D.,
 Tupy J.L., Bergman C., Beriman B., Carlson J.W., Celniker S.E.,
 Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
 Searle S.M.J., Smith E., Shu S., Smurniak F., Whitfield E.,
 Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 "Annotation of Drosophila melanogaster genome."
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [4]
 RN
 RP
 SEQUENCE FROM N.A.
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [5]
 RN
 RP
 SEQUENCE FROM N.A.
 RA FlyBase;
 RN
 RP
 Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF003686; AAN13464.1; -
 SQ SEQUENCE 348 AA; 38921 MW; 8FA837EF9A438134 CRC64;

 Query Match 59.9%; Score 45.5; DB 5; Length 348;
 Best Local Similarity 52.6%; Pred. No. 13;
 Matches 10; Conservative 0; Mismatches 2; Indels 7; Gaps 1;

 QY 1 YGG-----HQIYQFTDK 12
 Db 41 YGGVPSINSLHSIYQFQDK 59

 RESULT 5
 Q24544
 ID Q24544 PRELIMINARY; PRT; 388 AA.
 AC Q24544;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 16, Last annotation update)
 DE Homologous to synapsin II (Fragment).
 GN SYN OR SYN2 OR CG3395.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN
 RP
 SEQUENCE FROM N.A.
 RC STRAIN=WILDTYPE 'BERLIN'; TISSUE=Head;
 RX MEDLINE=96209149; PubMed=8627354;
 RA Klagges B.R., Heimbeck G., Godenschwege T.A., Hofbauer A.,
 Pflugfelder G.O., Reifegerste R., Reisch D., Schaupp M., Buchner S.,
 Buchner E.;
 RA "Invertebrate synapsins: a single gene codes for several isoforms in
 Drosophila";
 RT J. Neurosci. 16:3154-3165(1996).
 RL EMBL: X95454; CAA64724.1; -
 DR HSSP; P17599; 1AUX.
 DR FlyBase: FBgn004575; Syn.
 DR InterPro: IPR001359; Synapsin.
 DR Pfam: PF02078; Synapsin; 1.
 DR Pfam: PF02750; Synapsin_C; 1.
 DR PRINTS: PR01368; SYNAPSIN.
 FT NON_TER 1
 SQ SEQUENCE 388 AA; 42887 MW; 583B24E6456CBF40 CRC64;

Query Match 59.9%; Score 45.5; DB 5; Length 388;
 Best Local Similarity 52.6%; Pred. No. 15;
 Matches 10; Conservative 0; Mismatches 2; Indels 7; Gaps 1;

 QY 1 YGG-----HQIYQFTDK 12
 Db 81 YGGVPSINSLHSIYQFQDK 99

 RESULT 6
 Q9VH15
 ID Q9VH15 PRELIMINARY; PRT; 443 AA.
 AC Q9VH15;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE CG3985-PD.
 GN
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN
 RP
 SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 Abril J.F., Aghayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 Ballew R.W., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benos P.V., Beriman B.P., Bhandari D., Bolshakov S.,
 Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 Burkova K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.I., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 Spier E.C., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Svirkas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 Williams S.M., Woodruff, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 Yen R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [2]
 RN
 RP
 SEQUENCE FROM N.A.
 RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
 Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
 Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleeb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirkas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter C.J., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RP Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Gocayne J.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RP Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE FROM N.A.
RP FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; A003686; AAF54506.2; -
DR FlyBase; FBgn0004575; Syn.
SQ SEQUENCE 443 AA; 47645 MW; D1B10DA3E655C59D CRC64;
Query Match 59.9%; Score 45.5; DB 5; Length 443;
Best local Similarity 52.6%; Pred. No. 17;
Matches 10; Conservative 0; Mismatches 2; Indels 7; Gaps 1;
QY 1 YGG-----HQYQFTDK 12
DB 87 YGGVPSINSLSHSYQFDK 105
|||||
|||||
RESULT 7
Q8INM6 PRELIMINARY; PRT; 537 AA.
AC Q8INM6;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE CG3985-PB.
GN SYN.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA April J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrieli A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merklov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleeb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RN SEQUENCE FROM N.A.
RP Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Ananides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferrera S., Frise E., Galie R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleeb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirkas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter C.J., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RP Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RN SEQUENCE FROM N.A.
RP Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE FROM N.A.
RP FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; A003686; AAN13462.1; -
SQ SEQUENCE 537 AA; 57691 MW; 782BE20B4BE60220 CRC64;
Query Match 59.9%; Score 45.5; DB 5; Length 537;
Best local Similarity 52.6%; Pred. No. 21;
Matches 10; Conservative 0; Mismatches 2; Indels 7; Gaps 1;
QY 1 YGG-----HQYQFTDK 12
DB 181 YGGVPSINSLSHSYQFDK 199
|||||
|||||
RESULT 8
Q81050 PRELIMINARY; PRT; 776 AA.
ID 081050

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AC O81050;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE At2g03240 protein.
GN At2g03240.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10611797;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT thaliana."
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX STRAIN=cv. Columbia;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005313; AAC34478.1; -.
DR InterPro; IPR004342; EXS_Cterm.
DR InterPro; IPR004331; SPX.
DR Pfam; PF03124; EXS; 1.
DR Pfam; PF03105; SPX; 1.
SQ SEQUENCE 776 AA; 89775 MW; BE30603ACFADD014E CRC64;

Query Match 59.2%; Score 45; DB 10; Length 776;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGHQIYQFTDKD 13
DB 84 GGHQIGHFSDSD 95

RESULT 9
Q9X5R9
ID Q9X5R9 PRELIMINARY; PRT; 514 AA.
AC Q9X5R9;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MmCA.
GN MmCA.
OS Streptomyces lavendulae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1914;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL 2564;
RX MEDLINE=99201491; PubMed=10099135;
RA Mao Y., Varoglu M., Sherman D.H.;
RT "Molecular characterization and analysis of the biosynthetic gene
RT cluster for the antitumor antibiotic mitomycin C from Streptomyces
RT lavendulae NRRL 2564."
RL Chem. Biol. 6:251-263(1999).
DR EMBL; AF127374; AAD32724.1; -.
SQ SEQUENCE 514 AA; 55697 MW; 888C7E685882E2F CRC64;

Query Match 57.9%; Score 44; DB 2; Length 514;
Best Local Similarity 80.0%; Pred. No. 36;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGHQIYQFTD 11
DB 66 GGHQIYQFYD 75

RESULT 10
Q9ZKK7
ID Q9ZKK7 PRELIMINARY; PRT; 2231 AA.
AC Q9ZKK7;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Putative.
GN JHP0928.
OS Helicobacter pylori J99 (Campylobacter pylori J99).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=85963;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99120557; PubMed=9923682;
RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA Smith D.R., Noonan B., Guild B.C., DeJonge B.L., Carmel G.,
RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA Trust T.J.;
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori."
RL Nature 397:1176-180(1999).
DR EMBL; AE001522; AAD06506.1; -.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR002296; N12N6_mtfase.
DR InterPro; IPR000330; SNE2_N;
DR Pfam; PF00271; helicase_C; 1.
DR Pfam; PF00176; SNE2_N; 1.
DR PRINTS; PR00507; N12N6MTFRASE.
DR SMART; SM00487; DEXDg; 1.
DR SMART; SM00490; HELICc; 1.
KW Complete proteome.
SQ SEQUENCE 2231 AA; 255764 MW; 169B86503B7A2A8E CRC64;

Query Match 57.9%; Score 44; DB 16; Length 2231;
Best Local Similarity 53.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 YGGHQIYQFTDKD 13
DB 620 YGNHKIYSSNDKE 632

RESULT 11
Q8MXJ0
ID Q8MXJ0 PRELIMINARY; PRT; 173 AA.
AC Q8MXJ0;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein C08G9.1.
GN C08G9.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Waterston R.;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
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RX MEDLINE=95311309; PubMed=7540694;
RA Gardan R., Rapoport G., Debarbouille M.;
RT "Expression of the rocDEF operon involved in arginine catabolism in
RL Bacillus subtilis.";
RL J. Mol. Biol. 249:843-856(1995).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kasahara Y., Nakai S., Yoshikawa H., Ogasawara N.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Mosser I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertoletti M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borris R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruchi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinou S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Toseato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzengger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the gram-positive bacterium Bacillus
RL subtilis.";
RN Nature 390:249-256(1997).
RN [9]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; D78193; HAAL1297.1; -.
DR EMBL; Z99124; CAB16075.1; -.
KW Complete proteome.
SQ SEQUENCE 280 AA; 32594 MW; 991C958F77F58C77 CRC64;

Query Match 55.3%; Score 42; DB 16; Length 280;
Best Local Similarity 72.7%; Pred. No. 42;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGGHQIQYQFTD 11
Db 152 YEGHYIQYQTD 162

RESULT 14
Q9A5R9 PRELIMINARY; PRT; 324 AA.
AC Q9A5R9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE NAD-dependent epimerase/dehydratase family protein.
GN CC2378.

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OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Kolterbach T., Tran K., Wolf A., Vanathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL; AE005907; AK24349.1; -.
DR TIGR; CC2378; -.
DR InterPro; IPR001509; Epimerase_Dh.
DR Pfam; PF01370; Epimerase; 1.
KW Complete proteome.
SQ SEQUENCE 324 AA; 35414 MW; A5CB1D612F01EBDF CRC64;

Query Match 55.3%; Score 42; DB 16; Length 324;
Best Local Similarity 50.0%; Pred. No. 49;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGHQIQYQFTDKD 13
Db 244 GGHEVYNGDND 255

RESULT 15
Q8RCV8 PRELIMINARY; PRT; 326 AA.
AC Q8RCV8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Lipote-protein ligase A.
GN LPLA OR TTE0297.
OC Thermoanaerobacter tengcongensis.
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MB4 / JCM 11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
RA Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
RA Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL; AE013002; AAM23593.1; -.
DR InterPro; IPR004143; BPL_LipA_LipB.
DR InterPro; IPR004562; Lipoyltrans.
DR Pfam; PF03099; BPL_LipA_LipB; 1.
DR TIGRFAMs; TIGR00545; lipoyltrans; 1.
KW Ligase; Complete proteome.
SQ SEQUENCE 326 AA; 37543 MW; 2363F8E2F981D944 CRC64;

Query Match 55.3%; Score 42; DB 16; Length 326;
Best Local Similarity 50.0%; Pred. No. 49;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGHQIQYQFTDKD 13
Db 208 GGGEMVEFTED 219

Search completed: October 14, 2003, 08:40:16

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Tue Oct 14 10:50:38 2003

us-09-931-700-2.rspt

Page 8

Job time : 21.4318 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 08:34:01 ; Search time 52.1364 seconds
(without alignments)
94.378 Million cell updates/sec

Title: US-09-931-700-3

Perfect score: 163

Sequence: 1 TVOKLAHQIYQTDKDNVAPRSKISPOGY 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	163	100.0	31	18 AAW25160	Human preproadreno
2	163	100.0	31	22 AAB91762	Adrenomedullin pep
3	163	100.0	31	22 AAE09827	Human adrenomedull
4	163	100.0	52	22 AAB75110	Human adrenomedull
5	163	100.0	52	22 AAB91759	Adrenomedullin pep
6	163	100.0	52	22 AAE09818	Human adrenomedull
7	163	100.0	52	24 AAB55104	Human adrenomedull
8	163	100.0	53	22 AAB75111	Glycine extended h
9	163	100.0	53	22 AAB75112	Glycine extended a

10	163	100.0	53	24	ABJ18665	Universal stress p
11	163	100.0	62	22	AAB75113	Linker peptide-adr
12	163	100.0	120	22	AAB75122	UsPA(1-57)-(A)-(GS
13	163	100.0	120	22	AAB75123	UsPA(1-56)-(DD)-(G
14	163	100.0	120	24	ABJ18669	Universal stress p
15	163	100.0	120	24	ABJ18670	Universal stress p
16	163	100.0	147	22	AAB75124	UsPA(1-84)-(A)-(GS
17	163	100.0	147	24	ABJ18671	Universal stress p
18	163	100.0	170	22	AAB75114	Thioredoxin-(GSGSG
19	163	100.0	185	22	AAB49697	Human adrenomedull
20	163	100.0	185	22	AAB60344	Human adrenomedull
21	163	100.0	185	24	ABP72347	Adrenomedullin, in
22	163	100.0	206	24	ABJ18668	Adrenomedullin, in
23	157	96.3	188	22	AAB49698	Porcine adrenomedu
24	157	96.3	188	22	AAB60345	Porcine adrenomedu
25	148	90.8	40	22	AAB91768	Porcine adrenomedu
26	148	90.8	50	22	AAE09819	Adrenomedullin pep
27	148	90.8	185	22	AAB49699	Rat adrenomedullin
28	148	90.8	185	22	AAB60346	Rat adrenomedullin
29	140	85.9	184	23	ABBS7209	Rat adrenomedullin
30	136.5	83.7	53	22	AAB91767	Mouse ischaemic co
31	123.5	77.0	37	22	AAB91761	Adrenomedullin pep
32	123.5	75.8	52	22	AAB91765	Adrenomedullin pep
33	57	35.0	13	18	AAW25159	Human preproadreno
34	52	31.9	229	22	ABG05415	Novel human diagno
35	52	31.9	229	22	ABG13273	Novel human diagno
36	52	31.9	677	22	ABG09129	Novel human diagno
37	52	31.9	775	19	AAW56582	Novel human diagno
38	52	31.9	939	22	ABG14932	Kojibiose phosphor
39	52	31.9	994	22	ABG10411	Novel human diagno
40	51.5	31.6	620	23	ABP66343	Novel human diagno
41	51	31.3	10	15	AAW67024	Bifidobacterium lo
42	51	31.3	892	22	ABG62270	Hypotensive peptid
43	51	31.3	1096	22	ABG19648	Drosophila melanog
44	50	30.7	436	19	AAW56306	Novel human diagno
45	50	30.7	846	19	AAW56307	Clas I S-locus gly

ALIGNMENTS

RESULT 1
AAW25160
ID AAW25160 standard; peptide; 31 AA.

AC AAW25160;

DT 08-DEC-1997 (first entry)

XX Human preproadrenomedullin derived immunogen, P072.

XX Adrenomedullin; antibody; detection; diagnosis; cancer; renal; bone;
XX skin; blood related; disease; type II diabetes; preclampsia;
XX neurotransmission regulation; allergy; mast cell degranulation;
XX antibacterial; antifungal; wound repair.

OS Homo sapiens.

EH Key Location/Qualifiers

FT Peptide 1..31

FT Modified-site 31

FT /note= "residues 116-146 of preproadrenomedullin"

FT /note= "amidated"

XX WO9707214-A1.

XX 27-FEB-1997.

XX 16-AUG-1996; 96WO-US3286.

XX 12-MAR-1996; 96US-0013172.

PR 18-AUG-1995; 95US-0002514.

PR 30-AUG-1995; 95US-0002936.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Cuttitta F, Gray K, Hook W, Macri C, Martinez A;
 PI Miller MJ, Unsworth EJ, Walsh T;
 XX
 DR WPI; 1997-165298/15.
 XX
 XX Human adrenomedullin peptide(s), PO70, PO71, PO72 and PAMP-20 - used
 PT in the diagnosis and treatment of type II diabetes and cancer
 PT
 PS Claim 1; Page 43; 106pp; English.
 XX
 XX Human adrenomedullin (AM) peptides PO70, PO71, PO72 and PAMP-20
 CC were used for the production of anti-AM antibodies (Ab). PO70 represents
 CC preproAM amino acids (aa) 34-41 with the sequence Tyr-Tyr attached at
 CC the N-terminus, PO71 represents preproAM aa 122-131 with the sequence
 CC Tyr-Gly-Gly attached at the N-terminus, PO72 represents preproAM aa
 CC 116-146 and PAMP-20 represents the proAM N-terminus. The Ab are useful
 CC for the prevention and/or treatment of cancers, e.g. adrenal, nervous
 CC system, lung, colon, ovarian and breast cancer by inhibiting cell
 CC growth. They are also useful for regulating insulin secretion and blood
 CC glucose metabolism and therefore for treating and/or preventing diabetes
 CC type II. They may be used for the diagnosis or treatment of conditions
 CC relating to pregnancy e.g. preclampsia. The Ab are also useful
 CC for the following: (i) regulating neurotransmission or neuron growth in
 CC areas of the central nervous system; (ii) lessening or inhibiting mast
 CC cell degranulation and hence reducing the effects of an allergic
 CC response; (iii) inhibiting or preventing bacterial and fungal growth (to
 CC treat infection); (iv) facilitating wound healing; and (v) promoting
 CC organ and bone development.
 XX
 SQ Sequence 31 AA;
 Query Match 100.0%; Score 163; DB 18; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.9e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPOGY 31
 Db 1 TVQKLAHQIYQFTDKDKNVAPRSKISPOGY 31
 RESULT 2
 AAB91762
 ID AAB91762 standard; Peptide; 31 AA.
 XX
 AC AAB91762;
 DT 22-JUN-2001 (first entry)
 XX
 DE Adrenomedullin peptide (AM) SEQ ID NO:938.
 XX
 KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimide; maleimide group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200069900-A2.
 XX
 PD 23-NOV-2000.
 XX
 XX 17-MAY-2000; 2000WO-US13576.
 XX
 PR 17-MAY-1999; 99US-0134406.
 PR 10-SEP-1999; 99US-0153406.
 PR 15-OCT-1999; 99US-0159783.
 XX
 XX (CONJ-) CONJUCHEM INC.
 PA Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 PI

XX WPI; 2001-112059/12.
 DR
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PT
 XX
 PS Disclosure; Page 499-500; 733pp; English.
 XX
 XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (II) and a
 CC reactive group (III) (e.g. succinimide and maleimide groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 31 AA;
 Query Match 100.0%; Score 163; DB 22; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.9e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPOGY 31
 Db 1 TVQKLAHQIYQFTDKDKNVAPRSKISPOGY 31
 RESULT 3
 AAE09827
 ID AAE09827 standard; peptide; 31 AA.
 XX
 AC AAE09827;
 XX
 DT 29-NOV-2001 (first entry)
 XX
 DE Human adrenomedullin peptide #2.
 XX
 KW Human; vasoactive peptide; calcitonin gene related peptide; CGRP;
 KW CGRP-receptor identification; adrenomedullin.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Modified-site 31
 FT /note= "C-terminal amide"
 XX
 PN US6268474-B1.
 XX
 PD 31-JUL-2001.
 XX
 XX 30-APR-1998; 98US-0070504.
 PF
 XX 30-APR-1998; 98US-0070504.
 PR
 XX (UYCR-) UNIV CREIGHTON.
 XX
 PA Smith DD, Saha S, Abel PW;
 PI
 XX WPI; 2001-564216/63.
 XX
 XX Vasoactive peptides useful for inhibiting calcitonin gene related
 PT peptide receptor activity -

XX Claim 5; Column 6; 24pp; English.
 XX The invention relates to antagonists of the vasoactive peptide
 CC calcitonin gene related peptide (CGRP) and other members of the
 CC CGRP superfamily. The invention also relates to amino the terminal
 CC modifications of peptides to improve their ability to bind to a
 CC member of the CGRP-receptor super-family. CGRP antagonists are
 CC used for inhibiting CGRP activity which can be used in vitro e.g.
 CC in assays to identify and/or isolate CGRP receptors or with intact
 CC cells either in vitro or in vivo to inhibit the effect of CGRP
 CC binding to its receptor. The present sequence is human
 CC adrenomedullin peptide.

XX Sequence 31 AA;

Query Match 100.0%; Score 163; DB 22; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.9e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVOKLAHQIYQFTDKDKDNVAPRSKISPGY 31
 |||||
 Db 1 TVOKLAHQIYQFTDKDKDNVAPRSKISPGY 31

RESULT 4
 AAB75110
 ID AAB75110 standard; Protein; 52 AA.
 XX
 AC AAB75110;
 XX
 DT 31-JUL-2001 (first entry)
 XX
 DE Human adrenomedullin (AM) protein.
 XX
 KW Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;
 KW adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.
 XX
 OS Homo sapiens.
 XX
 PN WO200127310-A1.
 XX
 PD 19-APR-2001.
 XX
 PF 10-OCT-2000; 2000WO-JP07023.
 XX
 PR 15-OCT-1999; 99JP-0294147.
 XX
 PS (SHIO) SHIONOGI & CO LTD.
 XX
 PI Takimoto A, Mitsuda Y, Nakayama T, Mitsushima K;
 XX
 DR WPI; 2001-282044/29.
 DR N-PSDB; AAH19806.
 XX

PT Producing adrenomedullin useful for pharmaceutical and diagnostic
 PT application comprises producing fused adrenomedullin precursor using a
 PT recombinant host -
 XX
 PS Disclosure; Page 45; 75pp; Japanese.
 XX
 CC The present invention describes a method (M1) for producing
 CC adrenomedullin precursor. The method comprises: (a) producing the fused
 CC protein using a recombinant host cell; (b) restricted digestion of the
 CC fused protein by a protease followed by collection of sediment; and
 CC (c) dissolving the sediment and extracting adrenomedullin precursor.
 CC The method can be used for the production of adrenomedullin precursor
 CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866
 CC and AAB75110 to AAB75124 represent sequences which are used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 52 AA;

Query Match 100.0%; Score 163; DB 22; Length 52;
 Best Local Similarity 100.0%; Pred. No. 3.6e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVOKLAHQIYQFTDKDKDNVAPRSKISPGY 31

Query Match 100.0%; Score 163; DB 22; Length 52;
 Best Local Similarity 100.0%; Pred. No. 3.6e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVOKLAHQIYQFTDKDKDNVAPRSKISPGY 31
 |||||
 Db 22 TVOKLAHQIYQFTDKDKDNVAPRSKISPGY 52

RESULT 5
 AAB91759
 ID AAB91759 standard; Peptide; 52 AA.
 XX
 AC AAB91759;

XX 22-JUN-2001 (first entry)
 XX
 DE Adrenomedullin peptide (AM) SEQ ID NO:935.
 XX

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidy; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
 XX

OS Homo sapiens.
 OS Synthetic.

PN WO2000069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US13576.

XX 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity

XX Disclosure; Page 498; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidy and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.

XX Sequence 52 AA;

Query Match 100.0%; Score 163; DB 22; Length 52;
 Best Local Similarity 100.0%; Pred. No. 3.6e-18;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVOKLAHQIYQFTDKDKDNVAPRSKISPGY 31

DR N-PSDB; AAH19865.

PT Producing adrenomedullin useful for pharmaceutical and diagnostic

PT application comprises producing fused adrenomedullin precursor using a

PT recombinant host

XX

PS Claim 17; Page 69-70; 75pp; Japanese.

XX

CC The present invention describes a method (M1) for producing

CC adrenomedullin precursor. The method comprises: (a) producing the fused

CC protein using a recombinant host cell; (b) restricted digestion of the

CC fused protein by a protease followed by collection of sediment; and

CC (c) dissolving the sediment and extracting adrenomedullin precursor.

CC The method can be used for the production of adrenomedullin precursor

CC for pharmaceutical and diagnostic applications. AAH19806 to AAH19866

CC and AAB75110 to AAB75124 represent sequences which are used in the

CC exemplification of the present invention.

XX

SQ Sequence 120 AA;

Query Match 100.0%; Score 163; DB 22; Length 120;

Best Local Similarity 100.0%; Pred. No. 9.9e-18;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 31

DB 89 TVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 119

RESULT 14

ABJ18669

ID ABJ18669 standard; Protein; 120 AA.

AC ABJ18669;

XX 27-FEB-2003 (first entry)

DE Universal stress protein A (uspa)-related protein #4.

XX Fusion peptide; universal stress peptide; uspa; linker peptide;

KW large scale peptide production.

XX Unidentified.

OS WO200283907-A1.

XX 24-OCT-2002.

XX 04-APR-2002; 2002WO-JP03374.

XX 10-APR-2001; 2001JP-0111088.

XX (SHIO) SHIONOGI & CO LTD.

XX Mitsuda Y;

XX WPI; 2003-067581/06.

DR N-PSDB; ABT14529.

PT Fusion polypeptide of Escherichia coli universal stress peptide with a

PT target peptide, useful for efficient large scale production of the

PT target peptide comprising expression of the fusion polypeptide followed

PT by cleavage

XX Claim 5; Page 36; 49pp; Japanese.

XX

CC The invention comprises a novel fusion peptide which contains an

CC Escherichia coli universal stress protein (Uspa), a linker peptide and a

CC target peptide. The fusion protein is cleavable by a protease. The fusion

CC peptide of the invention is useful for the efficient large scale

CC production of peptides. The present amino acid sequence represents a

XX protein that was used in the invention.

SQ Sequence 120 AA;

Query Match 100.0%; Score 163; DB 24; Length 120;

Best Local Similarity 100.0%; Pred. No. 9.9e-18;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 31

DB 89 TVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 119

RESULT 15

ABJ18670

ID ABJ18670 standard; Protein; 120 AA.

XX ABJ18670;

XX 27-FEB-2003 (first entry)

DE Universal stress protein A (uspa)-related protein #5.

XX Fusion peptide; universal stress peptide; uspa; linker peptide;

KW large scale peptide production.

XX Unidentified.

OS WO200283907-A1.

XX 24-OCT-2002.

XX 04-APR-2002; 2002WO-JP03374.

XX 10-APR-2001; 2001JP-0111088.

XX (SHIO) SHIONOGI & CO LTD.

XX Mitsuda Y;

XX WPI; 2003-067581/06.

DR N-PSDB; ABT14530.

PT Fusion polypeptide of Escherichia coli universal stress peptide with a

PT target peptide, useful for efficient large scale production of the

PT target peptide comprising expression of the fusion polypeptide followed

PT by cleavage

XX Claim 5; Page 38; 49pp; Japanese.

XX

CC The invention comprises a novel fusion peptide which contains an

CC Escherichia coli universal stress protein (Uspa), a linker peptide and a

CC target peptide. The fusion protein is cleavable by a protease. The fusion

CC peptide of the invention is useful for the efficient large scale

CC production of peptides. The present amino acid sequence represents a

XX protein that was used in the invention.

SQ Sequence 120 AA;

Query Match 100.0%; Score 163; DB 24; Length 120;

Best Local Similarity 100.0%; Pred. No. 9.9e-18;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 31

DB 89 TVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 119

Search completed: October 14, 2003, 08:38:47

Job time : 53.1364 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 08:36:56 ; Search time 17,6136 Seconds
(without alignments)
169.257 Million cell updates/sec

Title: US-09-931-700-3
Perfect score: 163
Sequence: 1 TVQKLAHQYQFTDKDNVAPRSKISPGY 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	163	100.0	185	JN0684	adrenomedullin pre
2	157	96.3	188	S41500	adrenomedullin - p
3	146	90.8	185	JN0766	adrenomedullin pre
4	58.5	35.9	189	A99638	hypothetical prote
5	58.5	35.9	189	A85489	hypothetical prote
6	58	35.6	430	T14536	S-locus-specific g
7	56	34.4	431	T14415	S-locus-specific g
8	54	33.1	373	G84107	lipopolysaccharide
9	53	32.5	465	T15540	hypothetical prote
10	52	31.9	428	T14529	S-locus-specific g
11	51	31.3	428	T07814	S-locus-specific g
12	51	31.3	429	T14533	S-locus-specific g
13	51	31.3	436	A27827	S-locus-specific g
14	51	31.3	857	T14471	probable S-recepto
15	50	30.7	90	C86279	hypothetical prote
16	50	30.7	427	T14424	S-locus-specific g
17	50	30.7	428	T14423	S-locus-specific g
18	49	30.1	428	T14416	S-locus-specific g
19	49	30.1	428	T14530	S-locus-specific g
20	49	30.1	429	T07809	S-receptor kinase
21	49	30.1	429	T14528	S-locus-specific g
22	49	30.1	431	T07812	S-locus-specific g
23	49	30.1	431	T14418	S-locus-specific g
24	49	30.1	434	S04906	S-locus-specific g
25	48.5	29.8	322	T47067	hypothetical prote
26	48	29.4	328	T47067	probable cell divi
27	48	29.4	416	TJ3143	glycopeptide N-te
28	48	29.4	426	T07810	S-locus-specific g
29	48	29.4	444	E69130	histidine-trNA lig

30	48	29.4	689	2	S39531	excinuclease ABC c
31	48	29.4	856	1	JC2482	S-receptor kinase
32	48	29.4	858	1	JC2481	S-receptor kinase
33	48	29.4	1705	2	F71414	hypothetical prote
34	47.5	29.1	438	2	A55070	DNA primase (BC 2.
35	47	28.8	429	2	T14524	S-locus-specific g
36	47	28.8	545	2	A84938	flagellar M-ring p
37	47	28.8	549	2	T33517	hypothetical prote
38	47	28.8	850	2	T14472	S-receptor kinase
39	47	28.8	858	1	JQ1677	S-receptor kinase
40	47	28.8	1004	2	S51133	transposase ru4652
41	47	28.8	1268	2	A44125	high density lipop
42	47	28.8	1541	1	S71839	canalicular multidi
43	46.5	28.5	340	2	S41752	UDP-3-O-[3-hydroxy
44	46	28.2	186	2	H90448	hypothetical prote
45	46	28.2	204	2	C97389	hypothetical prote

ALIGNMENTS

RESULT 1

JN0684
adrenomedullin precursor - human
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000
C:Accession: JC2351; JN0684; P0548; JN0476
R:ishimitsu, T.; Kojima, M.; Kangawa, K.; Hino, J.; Matsuo, K.; Kitamura, K.; Eto,
Biochem. Biophys. Res. Commun. 203, 631-639, 1994
A:Title: Genomic structure of human adrenomedullin gene.
A:Reference number: JC2351; MUID:94354869; PMID:8074714
A:Accession: JC2351
A:Molecule type: DNA
A:Residues: 1-185 <ISH>
A:Cross-references: GB:S73906; NID:g765329; PIDN:AAC60642.1; PID:g765330
A:Experimental source: pheochromocytoma
R:Kitamura, K.; Sakata, J.; Kangawa, K.; Kojima, M.; Matsuo, H.; Eto, T.
Biochem. Biophys. Res. Commun. 194, 720-725, 1993
A:Title: Cloning and characterization of cDNA encoding a precursor for human adrenome
A:Reference number: JN0684; MUID:93343928; PMID:7668224
A:Accession: JN0684
A:Molecule type: mRNA
A:Residues: 1-185 <KIT>
A:Cross-references: GB:D14874; NID:g455470; PIDN:BAA03589.1; PID:g500612
A:Accession: P0548
A:Molecule type: protein
A:Residues: 22-41 <KIT>
R:Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Nakamura, S.; Matsuo, H.; Eto,
Biochem. Biophys. Res. Commun. 192, 553-560, 1993
A:Title: Adrenomedullin: A novel hypotensive peptide isolated from human pheochromocy
A:Reference number: JN0476; MUID:93249425; PMID:8367282
A:Accession: JN0476
A:Molecule type: protein
A:Residues: 95-146 <KIT>
A:Experimental source: pheochromocytoma
C:Genetics:
A:Gene: GDB:ADM
A:Cross-references: GDB:217070; OMIM:103275
A:Map position: 1pter-1lqter
A:Introns: 33/2; 83/2
C:Keywords: amidated carboxyl end; blood pressure control; hormone
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-185/Product: proadrenomedullin #status predicted <PEU>
F:22-41/Domain: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
F:95-146/Product: adrenomedullin #status experimental <MAR>
F:147-185/Domain: carboxyl-terminal propeptide #status predicted <CPT>
F:41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following
F:110-115/disulfide bonds: #status experimental
F:146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following

Query Match 100.0%; Score 163; DB 2: Length 185;
Best Local Similarity 100.0%; Pred. No. 2.3e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDNVAPRSKISPGY 31
 |||||
 Db 116 TVQKLAHQIYQFTDKDNVAPRSKISPGY 146

RESULT 2
 S41600
 adrenomedullin - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
 C:Accession: S41600
 R:Kitamura, K.; Kangawa, K.; Kojima, M.; Ichiki, Y.; Matsuo, H.; Eto, T.
 FEBS Lett. 338, 306-310, 1994
 A:Title: Complete amino acid sequence of porcine adrenomedullin and cloning of cDNA encoding the precursor
 A:Reference number: S41600; MUID:94139945; PMID:8043068
 A:Accession: S41600
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-188 <KIT>
 A:Cross-references: GB:D14875; NID:9439721; PIDN:BAA03590.1; PID:9496379

Query Match 96.3%; Score 157; DB 2; Length 188;
 Best Local Similarity 96.8%; Pred. No. 1,8e-15;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDNVAPRSKISPGY 31
 |||||
 Db 116 TVQKLAHQIYQFTDKDNVAPRSKISPGY 146

RESULT 3
 JN0766
 adrenomedullin precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 11-Jul-1997
 C:Accession: JN0766; P0610
 R:Sakata, J.; Shimokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, T.
 Biochem. Biophys. Res. Commun. 195, 921-927, 1993
 A:Title: Molecular cloning and biological activities of rat adrenomedullin, a hypotensive peptide
 A:Reference number: JN0766; MUID:93384621; PMID:7690563
 A:Accession: JN0766
 A:Molecule type: mRNA
 A:Residues: 1-185 <SAK>
 A:Accession: P0610
 A:Molecule type: protein
 A:Residues: 22-41 <SAZ>
 C:Comment: This precursor contains a unique 20-amino acid sequence designated proadrenomedullin
 C:Keywords: amidated carboxyl end
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-185/Product: proadrenomedullin #status predicted <PEU>
 F:22-41/Product: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>
 F:94-143/Product: adrenomedullin #status predicted <MAT>
 F:41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gly
 F:143/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gly

Query Match 90.8%; Score 148; DB 2; Length 185;
 Best Local Similarity 87.1%; Pred. No. 3.7e-14;
 Matches 27; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDNVAPRSKISPGY 31
 |||||
 Db 113 TVQKLAHQIYQFTDKDNVAPRSKISPGY 143

RESULT 4
 A99638
 hypothetical protein ECs0073 [imported] - Escherichia coli (strain O157:H7, substrain R1)
 C:Species: Escherichia coli
 C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
 C:Accession: A99638
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
 A:Reference number: A99629; MUID:21156231; PMID:11256796

A:Accession: A99638
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-189 <HAY>
 A:Cross-references: GB:BA000007; PIDN:BA033496.1; PID:gl3359529; GSPDB:GN00154
 A:Experimental source: strain O157:H7, substrain R1MD 0509952
 C:Genetics:
 A:Gene: ECs0073
 C:Superfamily: Escherichia coli yabp protein

Query Match 35.9%; Score 58.5; DB 2; Length 189;
 Best Local Similarity 34.4%; Pred. No. 0.5;
 Matches 11; Conservative 9; Mismatches 7; Indels 5; Gaps 1;

QY 4 KLAHQIYQFTD-----KDKDNVAPRSKISPG 30
 ||| : : : || : : : || : : : || :
 Db 95 KLTHWLKFNELKEYAKDPENNAKASLSPEG 126

RESULT 5
 A85489
 hypothetical protein 20078 [imported] - Escherichia coli (strain O157:H7, substrain E
 C:Species: Escherichia coli
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 C:Accession: A85489
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85489; MUID:21074935; PMID:11206551
 A:Accession: A85489
 A:Molecule type: DNA
 A:Status: preliminary
 A:Residues: 1-189 <STO>
 A:Cross-references: GB:AE005174; NID:gt12512769; PIDN:AAG54373.1; GSPDB:GN00145; UWGP:
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: 20078
 C:Superfamily: Escherichia coli yabp protein

Query Match 35.9%; Score 58.5; DB 2; Length 189;
 Best Local Similarity 34.4%; Pred. No. 0.5;
 Matches 11; Conservative 9; Mismatches 7; Indels 5; Gaps 1;

QY 4 KLAHQIYQFTD-----KDKDNVAPRSKISPG 30
 ||| : : : || : : : || : : : || :
 Db 95 KLTHWLKFNELKEYAKDPENNAKASLSPEG 126

RESULT 6
 T14536
 S-locus-specific glycoprotein - wild cabbage (fragment)
 N:Alternate names: S glycoprotein
 C:Species: Brassica oleracea (wild cabbage)
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000
 C:Accession: T14536
 R:Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
 Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
 A:Title: Striking sequence similarity in inter- and intra-specific comparisons of f cl
 mechanism.
 A:Reference number: Z18078; MUID:97352858; PMID:9207151
 A:Accession: T14536
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-430 <KUS>
 A:Cross-references: EMBL:D85212; NID:g2351155; PIDN:BAA21946.1; PID:g2351156
 C:Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
 C:Keywords: glycoprotein

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid C17C3.

A:Reference number: Z18366

A:Accession: T15540

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-465 <DUZ>

A:Cross-references: EMBL:U41279; NID:g1086905; PID:g1086919; PIDN:AAB52685.1; GSPDB:G1086919

A:Experimental source: strain Bristol N2; clone C17C3

C:Genetics:

A:Gene: CESP:C17C3.1

A:Map position: 2

A:Introns: 124/2; 138/2; 174/2; 223/1; 369/2

Query Match 32.5%; Score 53; DB 2; Length 465;

Best Local Similarity 40.0%; Pred. No. 8.7;

Matches 8; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 3 OKLAHOIYQFTDKDKDNVAP 22
||::: : ||: ||: |

DB 156 QEIAHKEFFDETELKDSFSP 175
||::: : ||: ||: |

RESULT 10

T14529

S-locus-specific glycoprotein - wild cabbage (fragment)

N:Alternate names: S glycoprotein

C:Species: Brassica oleracea (wild cabbage)

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Nov-2000

C:Accession: T14529

R:Kusaba, M.; Nishio, T.; Satta, Y.; Hinata, K.; Ockendon, D.
Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997

A:Title: Striking sequence similarity in inter- and intra-specific comparisons of a c1
echanism.

A:Reference number: Z18078; MUID:97352858; PMID:9207151

A:Accession: T14529

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-428 <SAK>

A:Cross-references: EMBL:D85205; NID:g2351141; PIDN:BAA21939.1; PID:g2351142

C:Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology

C:Keywords: glycoprotein

Query Match 31.9%; Score 52; DB 2; Length 428;

Best Local Similarity 28.2%; Pred. No. 11;

Matches 11; Conservative 8; Mismatches 10; Indels 10; Gaps 1;

QY 3 OKLAHOIYQFTDKDKD-----NVAPRKSIPQGY 31
||::: : ||: ||: |

DB 229 OKLSYMWYNTENSEVAFTFRNNFSYRLKVSDDGY 267
||::: : ||: ||: |

RESULT 11

T07814

S-locus-specific glycoprotein S6 - radish (fragment)

C:Species: Raphanus sativus (radish)

C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000

C:Accession: T07814

R:Sakamoto, K.; Kusaba, M.; Nishio, T.
Mol. Gen. Genet. 258, 397-403, 1998

A:Title: Polymorphism of the S-locus glycoprotein gene (SLG) and the S-locus related

A:Reference number: Z16146; MUID:98311079; PMID:9648745

A:Accession: T07814

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-428 <SAK>

A:Cross-references: EMBL:AB009682; NID:g3327849; PIDN:BAA31729.1; PID:g3327850

C:Genetics:

A:Gene: SLG(S6)

C:Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology

C:Keywords: glycoprotein

F:32-426/Domain: S-locus-specific glycoprotein homology <SSG>

Search completed: October 14, 2003, 08:40:50
Job time : 19.6136 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2003, 08:35:36 ; Search time 9.86364 Seconds
(without alignments)
147.798 Million cell updates/sec

Title: US-09-931-700-3
Perfect score: 163
Sequence: 1 TVQKLAHQIYQFTDKDNVAPRSKISPOGY 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	163	100.0	185	1	ADML_HUMAN
2	157	96.3	188	1	ADML_PIG
3	152	93.3	188	1	ADML_CANFA
4	148	90.8	185	1	ADML_RAT
5	146	89.6	188	1	ADML_BOVIN
6	140	85.9	184	1	ADML_MOUSE
7	51.5	31.6	620	1	ILV2_BIFLO
8	51	31.3	436	1	SLS6_BRAOL
9	49	30.1	180	1	VG48_BPMU
10	49	30.1	435	1	SLS2_BRAOA
11	48.5	29.8	322	1	Y4KA_RHLSN
12	48	29.4	328	1	ZIPA_YERPE
13	48	29.4	425	1	SYH_METH
14	48	29.4	496	1	NMT1_HUMAN
15	48	29.4	496	1	NMT1_MOUSE
16	48	29.4	497	1	NMT1_BOVIN
17	48	29.4	689	1	UVRA_PSELE
18	47.5	29.1	438	1	PRIL_DROME
19	47	28.8	545	1	FLIF_BUCAL
20	47	28.8	1268	1	VGLN_HUMAN
21	47	28.8	1541	1	MRP2_RAT
22	46.5	28.5	339	1	LPXD_YEREN
23	46.5	28.5	941	1	DNAB_RHOMR
24	46	28.2	434	1	SLS3_BRAOL
25	46	28.2	441	1	SPAC_BACSU
26	46	28.2	453	1	GATA_CAMIE
27	46	28.2	461	1	MIG6_MOUSE
28	46	28.2	922	1	YKFO_YEAST
29	46	28.2	1545	1	MRP2_HUMAN
30	46	28.2	4447	1	PKSK_BACSU
31	45	27.6	235	1	HG12_CAEEL
32	45	27.6	459	1	MIG6_RAT
33	45	27.6	576	1	SYPC_YEAST

34	45	27.6	599	1	FRDA_HAEIN
35	45	27.6	845	1	CC47_YEAST
36	45	27.6	2245	1	MYUJ_DICDI
37	45	27.6	2493	1	YBA4_YEAST
38	45	27.6	2778	1	FAF_DROME
39	45	27.6	3511	1	MY15_MOUSE
40	45	27.6	3530	1	MY15_HUMAN
41	44.5	27.3	136	1	GCS3_SULTO
42	44.5	27.3	426	1	YK96_AERPE
43	44.5	27.3	520	1	LAC1_AGABI
44	44.5	27.3	520	1	LAC2_AGABI
45	44.5	27.3	703	1	COAT_SMSV4

ALIGNMENTS

RESULT 1					
ID	ADML_HUMAN	STANDARD;	PRT;	185 AA.	
AC	P35318;				
DT	01-FEB-1994 (Rel. 28, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DT	15-SEP-2003 (Rel. 42, Last annotation update)				
DE	ADM precursor (Contains: Adrenomedullin (AM); Proadrenomedullin N-20 terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)).				
DE	ADM OR AM.				
GN	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
[1]					
RC	SEQUENCE FROM N.A.				
RC	TISSUE=Pheochromocytoma;				
RC	MEDLINE=93343928; Pubmed=7686224;				
RA	Kitamura K., Sakata J., Kangawa K., Kojima M., Matsuo H., Eto T.;				
RT	"Cloning and characterization of cDNA encoding a precursor for human adrenomedullin."				
RL	Biochem. Biophys. Res. Commun. 194:720-725(1993).				
[2]					
RC	SEQUENCE FROM N.A.				
RC	TISSUE=Liver;				
RC	MEDLINE=94354869; Pubmed=8074714;				
RA	Ishimitsu T., Kojima M., Kangawa K., Hino J., Matsuoka H.,				
RT	Kitamura K., Eto T., Matsuo H.;				
RL	"Genomic structure of human adrenomedullin gene."				
[3]					
RC	SEQUENCE FROM N.A.				
RC	TISSUE=Kidney;				
RC	MEDLINE=22388257; Pubmed=12477932;				
RA	Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,				
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,				
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,				
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,				
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,				
RA	Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,				
RA	Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,				
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,				
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,				
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;				
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."				
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).				
[4]					
RP	SEQUENCE OF 95-146.				

P44894	haemophilus
P38132	saccharomyc
P54697	dictyostell
P35194	saccharomyc
P55824	drosophila
Q9qz24	mus musculu
Q9ukn7	homo sapien
Q96z47	sulfolobus
Q9ya42	aeropyrum p
Q12541	agaricus bi
Q12542	agaricus bi
P36285	san mignuel

RC TISSUE-Pheochromocytoma;
 RX MEDLINE=93249425; PubMed=8387282;
 RA Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Nakamura S.,
 RA Matsuo H., Eto T.;
 RT "Adrenomedullin: a novel hypotensive peptide isolated from human
 RT pheochromocytoma.";
 RL Biochem. Biophys. Res. Commun. 192:553-560(1993).
 RN [5]
 RN REVIEW.
 RP RX MEDLINE=98240137; PubMed=9578982;
 RA Samson W.K.;
 RT "Proadrenomedullin-derived peptides.";
 RL Front. Neuroendocrinol. 19:100-127(1998).
 RN [6]
 RN REVIEW.
 RP RX MEDLINE=20053666; PubMed=10588445;
 RA Champion H.C., Nussdorfer G.G., Kadowitz P.J.;
 RT "Structure-activity relationships of adrenomedullin in the circulation
 RT and adrenal gland.";
 RL Regul. Pept. 85:1-8(1999).
 CC -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR
 CC AGENTS. NUMEROUS ACTIONS HAVE BEEN REPORTED MOST RELATED TO THE
 CC PHYSIOLOGIC CONTROL OF FLUID AND ELECTROLYTE HOMEOSTASIS. IN THE
 CC KIDNEY, AM IS DIURETIC AND NATRIURETIC, AND BOTH AM AND PAMP
 CC INHIBIT ALDOSTERONE SECRETION BY DIRECT ADRENAL ACTIONS. IN
 CC PITUITARY GLAND, BOTH PEPTIDES AT PHYSIOLOGICALLY RELEVANT DOSES
 CC INHIBIT BASAL ACTH SECRETION. BOTH PEPTIDES APPEAR TO ACT IN BRAIN
 CC AND PITUITARY GLAND TO FACILITATE THE LOSS OF PLASMA VOLUME,
 CC ACTIONS WHICH COMPLEMENT THEIR HYPOTENSIVE EFFECTS IN BLOOD
 CC VESSELS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN PHEOCHROMOCYTOMA AND
 CC ADRENAL MEDULLA. ALSO FOUND IN LUNG, VENTRICLE AND KIDNEY
 CC TISSUES.
 CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
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 CC
 CC EMBL; D14874; BAA03589.1;
 CC EMBL; S73906; AAC06042.1;
 CC EMBL; BC015961; AAH15961.1;
 CC EMBL; D43639; BAA07756.1; ALT_SEQ.
 CC PIR; JC2351; JN0684.
 CC Genew; HGNC:259; ADM.
 CC MIM; 103275;
 CC GO; GO:0005615; C:extracellular space; TAS.
 CC GO; GO:0003625; C:soluble fraction; TAS.
 CC GO; GO:0006171; P:CAMP biosynthesis; TAS.
 CC GO; GO:0007267; P:cell-cell signaling; TAS.
 CC GO; GO:0008015; P:circulation; TAS.
 CC GO; GO:0007565; P:pregnancy; TAS.
 CC GO; GO:0006701; P:progesterone biosynthesis; TAS.
 CC GO; GO:0009611; P:response to wounding; TAS.
 CC GO; GO:0007165; P:signal transduction; TAS.
 CC InterPro; IPR001710; Adrenomedullin.
 CC Pfam; PF02039; Adrenomedullin; 1.
 CC DR PRINTS; PR00801; ADRENOMEDULLIN.
 CC Hormone; Amidation; Cleavage on pair of basic residues; Signal;
 CC Polymorphism.
 CC SIGNAL 1 21 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
 CC PEPTIDE 22 41
 CC PROPEP 45 92
 CC PEPTIDE 95 146 ADRENOMEDULLIN.
 CC PROPEP 148 185 PREPROAM C-TERMINAL FRAGMENT.
 CC PEPTIDE 110 115
 CC DISULFID 41 41 AMIDATION (G-42 PROVIDE AMIDE GROUP).
 CC MOD_RES 146 146 AMIDATION (G-147 PROVIDE AMIDE GROUP).

FT VARIANT 50 50 S -> R (in dbSNP:5005).
 FT /FtId=VAR_014861.
 SQ SEQUENCE 185 AA; 20420 MW; 64C7D2A0B4654DFE CRC64;
 Query Match 100.0%; Score 163; DB 1; Length 185;
 Best local Similarity 100.0%; Pred. NO. 4.2e-16;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TVOKLAHQIYQFTDKDKDNVAPRSKISPOGY 31
 Db 116 TVOKLAHQIYQFTDKDKDNVAPRSKISPOGY 146
 RESULT 2
 ADML_PIG STANDARD; PRT; 188 AA.
 ID ADML_PIG
 AC P33366;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
 DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
 GN ADM OR AM.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Adrenal medulla;
 RA KITAMURA K., KANGAWA K., KOJIMA M., ICHIKI Y., MATSUO H., ETO T.;
 RX MEDLINE=94139945; PubMed=8043068;
 RT "Complete amino acid sequence of porcine adrenomedullin and cloning
 RT of cDNA encoding its precursor.";
 RL FEBS Lett. 338:306-310(1994).
 RN [2]
 RP SEQUENCE OF 22-41.
 RC TISSUE-Adrenal medulla;
 RX MEDLINE=94357274; PubMed=8076689;
 RA KITAMURA K., KANGAWA K., ISHIYAMA Y., WASHIMINE H., ICHIKI Y.,
 RA KAWAMOTO M., MINAMINO N., MATSUO H., ETO T.;
 RT "Identification and hypotensive activity of proadrenomedullin
 RT N-terminal 20 peptide (PAMP).";
 RL FEBS Lett. 351:35-37(1994).
 CC -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR
 CC AGENTS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN ADRENAL GLANDS, LUNG, AND
 CC KIDNEY
 CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
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 CC EMBL; D14875; BAA03590.1;
 CC PIR; S41600; S41600.
 CC InterPro; IPR001710; Adrenomedullin.
 CC Pfam; PF02039; Adrenomedullin; 1.
 CC PRINTS; PR00801; ADRENOMEDULLIN.
 CC Hormone; Amidation; Cleavage on pair of basic residues; Signal.
 CC SIGNAL 1 21 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
 CC PEPTIDE 22 41
 CC PROPEP 45 92
 CC PEPTIDE 95 146 ADRENOMEDULLIN.
 CC PROPEP 153 188 PREPROAM C-TERMINAL FRAGMENT (BY
 CC SIMILARITY).
 CC DISULFID 110 115 BY SIMILARITY.
 CC MOD_RES 41 41 AMIDATION (G-42 PROVIDE AMIDE GROUP).

FT MOD_RES 146 146 AMIDATION (G-147 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 188 AA; 20893 MW; 71749460F5660A61 CRC64;

Query Match
 Best Local Similarity 96.3%; Score 157; DB 1; Length 188;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 31
 Db 116 TVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 146

RESULT 3
 ADML_CANFA STANDARD; PRT; 188 AA.
 ID ADML_CANFA
 AC 077559; Q9TVC9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
 DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
 GN ADM.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Imoto I., Jougasaki M.;
 RT "Cloning of cDNA encoding canine adrenomedullin.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99002704; PubMed=9788655;
 RA Ono Y., Kojima M., Okada K., Kangawa K.;
 RT "cDNA cloning of canine adrenomedullin and its gene expression in the
 RT heart and blood vessels in endotoxin shock.";
 RL Shock 10:243-247(1998).
 CC -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR
 CC AGENTS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
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 CC EMBL; AF045773; AAD05423.1; -;
 CC EMBL; U96127; AAD09957.1; -;
 CC InterPro; IPR001710; Adrenomedullin.
 CC Pfam; PF02039; Adrenomedullin; 1.
 CC PRINTS; PR00801; ADRENOMEDULLIN.
 CC Hormone; Amidation; Cleavage on pair of basic residues; Signal.
 CC SIGNAL 1 21 BY SIMILARITY.
 CC FT PEPTIDE 22 41 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
 CC FT PROPEP 45 92 BY SIMILARITY.
 CC FT PEPTIDE 95 146 ADRENOMEDULLIN.
 CC FT PROPEP 148 188 PREPROAM C-TERMINAL FRAGMENT (BY
 CC SIMILARITY).
 CC FT DISULFID 110 115 BY SIMILARITY.
 CC FT MOD_RES 41 41 AMIDATION (G-42 PROVIDE AMIDE GROUP)
 CC (BY SIMILARITY).
 CC FT MOD_RES 146 146 AMIDATION (G-147 PROVIDE AMIDE GROUP)
 CC (BY SIMILARITY).
 CC FT CONFLICT 130 130 N -> K (IN REF. 2).
 CC FT SEQUENCE 188 AA; 20929 MW; 809D6A64F96F578 CRC64;
 CC
 CC Query Match
 CC Best Local Similarity 93.3%; Score 152; DB 1; Length 188;
 CC Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 31
 Db 116 TVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 146

RESULT 4
 ADML_RAT STANDARD; PRT; 185 AA.
 ID ADML_RAT
 AC P43145;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
 DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
 GN ADM.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Adrenal gland;
 RX MEDLINE=93384621; PubMed=7690563;
 RA Sakata J., Shimokuba T., Kitamura K., Kangawa K.,
 RA Matsuo H., Eto T.;
 RT "Molecular cloning and biological activities of rat adrenomedullin, a
 RT hypotensive peptide.";
 RL Biochem. Biophys. Res. Commun. 195:921-927(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96102137; PubMed=8524787;
 RA Wang X., Yue T.L., Barone F.C., White R.F., Clark R.K., Willette R.N.,
 RA Sulprizio A.C., Aiyar N.V., Ruffolo R.R. Jr., Feuerstein G.Z.;
 RT "Discovery of adrenomedullin in rat ischemic cortex and evidence for
 RT its role in exacerbating focal brain ischemic damage.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:11480-11484(1995).
 CC -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR
 CC AGENTS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ADRENAL GLANDS, LUNG, KIDNEY,
 CC HEART, SPLEEN, DUODENUM AND SUBMANDIBULAR GLANDS.
 CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.
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 CC
 CC EMBL; D15069; BAA03665.1; -;
 CC EMBL; U15419; AAB60519.1; -;
 CC InterPro; IPR001710; Adrenomedullin.
 CC Pfam; PF02039; Adrenomedullin; 1.
 CC PRINTS; PR00801; ADRENOMEDULLIN.
 CC Hormone; Amidation; Cleavage on pair of basic residues; Signal.
 CC SIGNAL 1 21 BY SIMILARITY.
 CC FT PEPTIDE 22 41 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
 CC FT PROPEP 45 91 BY SIMILARITY.
 CC FT PEPTIDE 94 143 ADRENOMEDULLIN.
 CC FT PROPEP 149 185 PREPROAM C-TERMINAL FRAGMENT (BY
 CC SIMILARITY).
 CC FT DISULFID 107 112 BY SIMILARITY.
 CC FT MOD_RES 41 41 AMIDATION (G-42 PROVIDE AMIDE GROUP)
 CC (BY SIMILARITY).
 CC FT MOD_RES 143 143 AMIDATION (G-144 PROVIDE AMIDE GROUP)
 CC (BY SIMILARITY).
 CC FT SEQUENCE 185 AA; 20636 MW; 35CAD9A9DD19AE35 CRC64;

Query Match 90.8%; Score 148; DB 1; Length 185;
 Best Local Similarity 87.1%; Pred. No. 5.7e-14;
 Matches 27; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVOKLAHQIYQFTDKDNVAPRSKISPGY 31
 |:|||||:|||||:|||||:|||||:|||||
 DB 113 TMQKLAHQIYQFTDKDNVAPRSKISPGY 143

RESULT 5

ADML_BOVIN
 ID ADML_BOVIN STANDARD; PRT; 188 AA.
 AC 062827;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
 DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
 GN ADM.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Aorta;
 RX MEDLINE=98244567; PubMed=9585168;
 RA Barker S., Wood E., Clark A.J.L., Corder R.;
 RA "Cloning of bovine proadrenomedullin and inhibition of its basal
 RT expression in vascular endothelial cells by staurosporine.";
 RL Life Sci. 62:1407-1415(1998).
 CC -1- FUNCTION: HYPOTENSIVE PEPTIDE. MAY FUNCTION AS A HORMONE IN
 CC CIRCULATION CONTROL (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.

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 CC -----

EMBL: AJ001613; CRA04866.1; -
 DR InterPro: IPR001710; Adrenomedullin.
 DR Pfam: PF02039; Adrenomedullin; 1.
 DR PRINTS; PR00801; ADRENOMEDULLIN.
 KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT PEPTIDE 22 41 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
 FT PROPEP 45 92 BY SIMILARITY.
 FT PEPTIDE 95 146 ADRENOMEDULLIN.
 FT PROPEP 148 188 PREPROAM C-TERMINAL FRAGMENT (BY
 FT SIMILARITY).
 FT DISULFID 110 115 BY SIMILARITY.
 FT MOD_RES 41 41 AMIDATION (G-42 PROVIDE AMIDE GROUP)
 FT (BY SIMILARITY).
 FT MOD_RES 146 146 AMIDATION (G-147 PROVIDE AMIDE GROUP)
 FT (BY SIMILARITY).
 SQ SEQUENCE 188 AA; 20981 MW; 3002E79AB3B6612C CRC64;

Query Match 89.6%; Score 146; DB 1; Length 188;
 Best Local Similarity 90.3%; Pred. No. 1.1e-13;
 Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TVOKLAHQIYQFTDKDNVAPRSKISPGY 31
 |:|||||:|||||:|||||:|||||:|||||
 DB 116 TVOKLAHQIYHFTDKDNVAPRSKISPGY 146

RESULT 6

ADML_MOUSE
 ID ADML_MOUSE STANDARD; PRT; 184 AA.
 AC P97297; P97453;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20
 DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].
 GN ADM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=97092892; PubMed=8938454;
 RA Okazaki T., Ogawa Y., Tamura N., Mori Y., Isse N., Aoki T.,
 RA Rochelle J.M., Taketo M.M., Seldin M.F., Nakao K.;
 RA "Genomic organization, expression, and chromosomal mapping of the
 RT mouse adrenomedullin gene.";
 RL Genomics 37:395-399(1996).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC STRAIN=C57BL/6J;
 CC MEDLINE=99046755; PubMed=9808778;
 CC Yotsumoto S., Shimada T., Cui C.Y., Nakashima H., Fujiwara H.,
 CC Ko M.S.H.;
 CC "Expression of adrenomedullin, a hypotensive peptide, in the
 RT trophoblast giant cells at the embryo implantation site in mouse.";
 RL Dev. Biol. 203:264-275(1998).
 CC -1- FUNCTION: AM AND PAMP ARE POTENT HYPOTENSIVE AND VASODILATOR
 CC AGENTS.

 CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: BELONGS TO THE ADRENOMEDULLIN FAMILY.

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 CC -----

EMBL: D78349; BAA11367.1; -
 DR EMBL; U77630; AAB36535.1; -
 DR MGD; MGI:108058; Adm.
 DR InterPro: IPR001710; Adrenomedullin.
 DR Pfam: PF02039; Adrenomedullin; 1.
 DR PRINTS; PR00801; ADRENOMEDULLIN.
 KW Hormone; Amidation; Cleavage on pair of basic residues; Signal.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT PEPTIDE 22 41 PROADRENOMEDULLIN N-20 TERMINAL PEPTIDE.
 FT PROPEP 45 92 BY SIMILARITY.
 FT PEPTIDE 95 144 ADRENOMEDULLIN.
 FT PROPEP 151 184 PREPROAM C-TERMINAL FRAGMENT (BY
 FT SIMILARITY).
 FT DISULFID 108 113 BY SIMILARITY.
 FT MOD_RES 41 41 AMIDATION (G-42 PROVIDE AMIDE GROUP)
 FT (BY SIMILARITY).
 FT MOD_RES 144 144 AMIDATION (G-145 PROVIDE AMIDE GROUP)
 FT (BY SIMILARITY).
 FT CONFLICT 173 173 A -> G (IN REF. 2).
 FT SEQUENCE 184 AA; 20764 MW; C88C99045A79C898 CRC64;

Query Match 85.9%; Score 140; DB 1; Length 184;
 Best Local Similarity 83.9%; Pred. No. 7.9e-13;
 Matches 26; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 TVOKLAHQIYQFTDKDNVAPRSKISPGY 31
 |:|||||:|||||:|||||:|||||:|||||
 DB 114 TVOKLAHQIYQFTDKDNVAPRSKISPGY 144


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RESULT 7
ILVD_BIFLO
ID ILVD_BIFLO STANDARD; PRT; 620 AA.
AC QG3H2;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DE Dihydroxy-acid dehydratase (EC 4.2.1.9) (DAD).
GN ILVD OR BL1788.
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 2705;
RX MEDLINE=2294977; PubMed=12381787;
RA Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
RA Pessi G., Zwaalen M.-C., Desiere F., Bork P., Delley M.,
RA Pridmore R.D., Arigoni F.
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract.;"
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
CC -1- CATALYTIC ACTIVITY: 2,3-dihydroxy-3-methylbutanoate = 3-methyl-2-
CC oxobutanoate + H(2)O.
CC -1- COFACTOR: Binds 1 4Fe-4S cluster (Potential).
CC -1- PATHWAY: Valine and isoleucine biosynthesis; fourth step.
CC -1- SIMILARITY: BELONGS TO THE ILVD / EDD FAMILY.
CC -----
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CC -----
CC EMBL; AE014813; AAN25571.1; -
CC HAMAP; MF_00012; -; 1.
CC ProDom; PD002691; ILVD_EDD_family; 1.
CC TIGRfams; TIGR00110; ILVD; 1.
CC PROSITE; PS00886; ILVD_EDD_1; 1.
CC PROSITE; PS00887; ILVD_EDD_2; FALSE NEG.
CC Branched-chain amino acid biosynthesis; Lyase; Iron; Iron-sulfur;
CC 4Fe-4S; Complete proteome.
CC METAL 123 123 IRON-SULFUR (4FE-4S) (POTENTIAL).
CC METAL 197 197 IRON-SULFUR (4FE-4S) (POTENTIAL).
CC SEQUENCE 620 AA; 66557 MW; 463F654306027ABE CRC64;

Query Match 31.6%; Score 51.5; DB 1; Length 620;
Best Local Similarity 40.0%; Pred. No. 12;
Matches 12; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

QY 2 VQLAHQIYQFTDKDNVAPRSKISPGQY 31
| : ||| | | : ||| : :
241 VVKIAHOY---DSDSDVLPRTATKEAF 267

RESULT 8
SLSG6_BRAOL
ID SLSG6_BRAOL STANDARD; PRT; 436 AA.
AC P07761;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE S-locus-specific glycoprotein S6 precursor (SLSG-6).
GN SLSG.
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

Query Match 31.3%; Score 51; DB 1; Length 436;
Best Local Similarity 25.6%; Pred. No. 9.5;
Matches 10; Conservative 10; Mismatches 9; Indels 10; Gaps 1;

QY 3 QKLAHQIYQFTDKDKD-----NVAPRSKISPGQY 31
| : ||| | | : ||| : :
237 QKLSYMYNFTENSEEVAYTFRTNNSIYSLTSLSEGY 275

RESULT 9
VG48_BPMU
ID VG48_BPMU STANDARD; PRT; 180 AA.
AC Q9T1V1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein gp48.

eurosid II; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID=3712;
RN [1]
RP SEQUENCE FROM N.A.
RA Nasrallah J.B., Kao T.-H., Chen C.H., Goldberg M.L., Nasrallah M.E.;
RT "Amino-acid sequence of glycoproteins encoded by three alleles of the
RT S locus of Brassica oleracea.;"
RL Nature 326:617-619(1987).
RN [2]
RP SEQUENCE OF 22-435 FROM N.A.
RA Nasrallah J.B., Kao T.-H., Goldberg M.L., Nasrallah M.E.;
RT "A cDNA clone encoding an S-locus-specific glycoprotein from Brassica
RT oleracea.;"
RL Nature 318:263-267(1985).
RN [3]
RP ERRATUM.
RA Nasrallah J.B., Kao T.-H., Goldberg M.L., Nasrallah M.E.;
RL Nature 326:523-523(1987).
CC -1- FUNCTION: INVOLVED IN SPOROPHYTIC SELF-INCOMPATIBILITY SYSTEM
CC (THE INABILITY OF FLOWERING PLANTS TO ACHIEVE SELF-FERTILIZATION).
CC -1- TISSUE SPECIFICITY: STIGMA.
CC -1- POLYMORPHISM: THERE ARE A TOTAL OF 50 DIFFERENT S ALLELES IN
CC B.OLERACEA.
CC -1- SIMILARITY: TO THE EXTRACELLULAR PORTION OF A MAIZE PROTEIN
CC KINASE RECEPTOR (ZMPK1).
CC -----
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CC -----
CC EMBL; Y00268; CAA68375.1; -
CC EMBL; X03170; CAA26934.1; ALT_INIT.
CC PIR; A27827; A27827.
CC InterPro; IPR001480; B_lectin.
CC InterPro; IPR003609; Pan_app.
CC InterPro; IPR000858; Slocus_glycop.
CC Pfam; PF01453; Agglutinin; 1.
CC Pfam; PF00954; S-locus-glycop; 1.
CC SMART; SM00108; B_lectin; 1.
CC SMART; SM00473; PAN_AP; 1.
CC Self-incompatibility; Glycoprotein; Polymorphism; Signal.
CC SIGNAL 1 31
CC CHAIN 32 436
CC CARBOHYD 46 46 S-LOCUS-SPECIFIC GLYCOPROTEIN S6.
CC CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 245 245 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 436 AA; 49779 MW; E2332635885A515 CRC64;

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DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cell division protein zipA homolog.
DE ZIPA OR IF02990 OR IF1491.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Varra A.M.,
RA Chillingworth T., Cronin A., Davies K.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague."
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Retherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM."
RL J. Bacteriol. 184:4601-4611(2002).
CC -1- FUNCTION: Interacts directly with the cell division protein ftsZ.
CC Probable receptor for the septal ring structure, may anchor it
CC to the inner-membrane (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane (By
CC similarity).
CC -1- SIMILARITY: Belongs to the zipA family.
CC -----
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CC -----
DR EMBL; AJ141454; CAC92234.1; -
DR EMBL; AE013752; AM85062.1; ALT_INIT.
DR PIR; AG0363; AG0363.
DR HAMAP; MF_00509; -.
DR Pfam; PF04354; ZipA_C; 1.
DR Cell division; Septation; Transmembrane; Inner membrane;
DR KW Complete proteome.
FT DOMAIN 1 4 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 5 25 POTENTIAL.
FT DOMAIN 26 328 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 328 AA; 36098 MW; EA04B89084649044 CRC64;

Query Match 29.4%; Score 48; DB 1; Length 328;
Best Local Similarity 36.7%; Pred. No. 19;
Matches 11; Conservative 6; Mismatches 11; Indels 2; Gaps 1;

QY 2 VKLAHQI--YQFTDKDKNVAPRSKISQ 29
Db 156 VERPAHQVAPQHQVESQEPVAPAKPQ 195

RESULT 13
SYN_METH ID SYN_METHTH PRT; 425 AA.
AC 026346;

DT 15-JUL-1998 (Rel. 36, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
DE (HisRS).
DE ZISA OR IF02990 OR IF1491.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucet-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RL J. Bacteriol. 179:7135-7155(1997).
CC -1- CATALYTIC ACTIVITY: ATP + L-histidine + tRNA(His) -> AMP +
CC diphosphate + L-histidyl-tRNA(His).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
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CC -----
DR EMBL; AE000811; AAB84750.1; ALT_INIT.
DR HSP; O32422; IQE0.
DR HAMAP; MF_00127; 1.
DR InterPro; IPR004154; HGTP_anticonodon.
DR InterPro; IPR004516; HisS.
DR InterPro; IPR002314; tRNA-synt_2b.
DR InterPro; IPR006195; tRNA_ligase_II.
DR Pfam; PF03129; HGTP_anticonodon; 1.
DR Pfam; PF00587; tRNA-synt_2b; 1.
DR TIGR; TIGR00442; hisS; 1.
DR PROSITE; PS00862; AA_TRNA_LIGASE_II; 1.
DR Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
DR KW Complete proteome.
SQ SEQUENCE 425 AA; 48019 MW; 8388A5975A017535 CRC64;

Query Match 29.4%; Score 48; DB 1; Length 425;
Best Local Similarity 36.0%; Pred. No. 25;
Matches 9; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 3 OKLAHQIYQFTDKDKNVAPRSKIS 27
Db 56 EVVNVQIYHFTDKGRELALRLT 80

RESULT 14
NM1_HUMAN STANDARD; PRT; 496 AA.
AC P30419;
DT 01-APR-1993 (Rel. 25, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Glycylpeptide N-tetradecanoyltransferase 1 (EC 2.3.1.97) (peptide N-
DE myristoyltransferase 1) (Myristoyl-CoA:protein N-myristoyltransferase
DE 1) (NMT 1) (Type 1 N-myristoyltransferase).
GN NM1 OR NMT.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RP [1]
 RP SEQUENCE OF 58-496 FROM N.A., AND MUTAGENESIS OF GLY-492.
 RX MEDLINE=92237320; PubMed=15703339;
 RA Duronio R.J., Reed S.I., Gordon J.I.;
 RA "Mutations of human myristoyl-CoA:protein N-myristoyltransferase
 RT cause temperature-sensitive myristic acid auxotrophy in *Saccharomyces*
 RT *cerevisiae*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:4129-4133(1992).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=98019247; PubMed=9353336;
 RA Glover C.J., Hartman K.D., Felsted R.L.;
 RA "Human N-myristoyltransferase amino-terminal domain involved in
 RT targeting the enzyme to the ribosomal subcellular fraction.";
 RL J. Biol. Chem. 272:28680-28689(1997).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RX MEDLINE=98175914; PubMed=9506952;
 RA Giang D.K., Cravatt B.F.;
 RA "A second mammalian N-myristoyltransferase.";
 RL J. Biol. Chem. 273:6595-6598(1998).
 RN [4]
 RN SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
 RC TISSUE=Muscle, and Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.K., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RN SEQUENCE OF 81-89 FROM N.A.
 RX MEDLINE=98343933; PubMed=9677304;
 RA McIlhinney R.A.J., Young K., Egerton M., Camble R., White A.,
 RA Soloviev M.;
 RA "Characterization of human and rat brain myristoyl-CoA:protein
 RT N-myristoyltransferase: evidence for an alternative splice variant of
 RT the enzyme.";
 RL Biochem. J. 333:491-495(1998).
 CC -!- FUNCTION: Adds a myristoyl group to the N-terminal glycine residue
 CC of certain cellular and viral proteins.
 CC -!- CATALYTIC ACTIVITY: Tetradecanoyl-CoA + glycyl-peptide = CoA + N-
 CC tetradecanoylglycyl-peptide.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=Long;
 CC IsoId=P30419-1; Sequence=Displayed;
 CC Name=Short;
 CC IsoId=P30419-2; Sequence=VSP_003570;
 CC -!- TISSUE SPECIFICITY: HEART, GUT, KIDNEY, LIVER, AND PLACENTA.
 CC -!- SIMILARITY: BELONGS TO THE NMT FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; MB6707; -; NOT ANNOTATED CDS.
 DR EMBL; AF043324; AAC0294.1; ALT_INIT.
 DR EMBL; AF020500; AAB95316.1; -;
 DR EMBL; BC006538; AAH06538.1; -;
 DR EMBL; BC006569; AAH06569.1; -;
 DR EMBL; BC007258; AAH07258.1; -;
 DR EMBL; BC008312; AAH08312.1; -;
 DR EMBL; Y17209; CAA76686.1; -;
 DR FIR; JCI343; JCI343.
 DR HSSP; P30418; INMT.
 DR Genew; HGNC:7857; NMT1.
 DR MIM; 160993; -;
 DR GO; GO:0009249; P:protein-lipoylation; TAS.
 DR InterPro; IPR000903; Nmt.
 DR Pfam; PF01233; NMT_1.
 DR Pfam; PF02799; NMT_C; 1.
 DR PROSITE; PS00975; NMT_1; 1.
 DR PROSITE; PS00976; NMT_2; 1.
 KW Transferase; Acyltransferase; Alternative splicing.
 FT DOMAIN 55 67
 FT VARSPLIC 1 80
 FT MISSING (in isoform Short).
 FT MUTAGEN 492 492 /FTID-VSP_003570.
 FT G->D,K: REDUCED ACTIVITY.
 SQ SEQUENCE 496 AA; 56806 MW; 7661140D3837BE7A CRC64;
 Query Match 29.4%; Score 48; DB 1; Length 496;
 Best Local Similarity 24.5%; Pred. No. 29;
 Matches 12; Conservative 7; Mismatches 12; Indels 18; Gaps 1;
 QY 1 TVQKLAHQIYQFTD-----KDKDNVAPRSKISPGY 31
 Db 108 TWEEASKRSYQFWDTPQPKLGEVNVTHGVPDPKDNIRQEPYTLPGF 156
 RESULT 15
 NMT1_MOUSE
 ID NMT1_MOUSE STANDARD; PRT; 496 AA.
 AC 070310;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Glycylpeptide N-tetradecanoyltransferase 1 (EC 2.3.1.97) (peptide N-
 DE myristoyltransferase 1) (Myristoyl-CoA:protein N-myristoyltransferase
 DE 1) (NMT 1) (Type I N-myristoyltransferase).
 GN NMT1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=98175914; PubMed=9506952;
 RA Giang D.K., Cravatt B.F.;
 RA "A second mammalian N-myristoyltransferase.";
 RL J. Biol. Chem. 273:6595-6598(1998).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.K., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
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 RT human and mouse cDNA sequences.";
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 RA "Characterization of human and rat brain myristoyl-CoA:protein
 RT N-myristoyltransferase: evidence for an alternative splice variant of
 RT the enzyme.";
 RL Biochem. J. 333:491-495(1998).
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 CC -!- CATALYTIC ACTIVITY: Tetradecanoyl-CoA + glycyl-peptide = CoA + N-
 CC tetradecanoylglycyl-peptide.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=Long;
 CC IsoId=P30419-1; Sequence=Displayed;
 CC Name=Short;
 CC IsoId=P30419-2; Sequence=VSP_003570;
 CC -!- TISSUE SPECIFICITY: HEART, GUT, KIDNEY, LIVER, AND PLACENTA.
 CC -!- SIMILARITY: BELONGS TO THE NMT FAMILY.
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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahay J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Brakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Adds a myristoyl group to the N-terminal glycine residue
CC of certain cellular and viral proteins.
CC -1- CATALYTIC ACTIVITY: tetradecanoyl-CoA + glycyl-peptide = CoA + N-
CC tetradecanoylglycyl-peptide.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE NMT FAMILY.
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CC -----
DR EMBL; AF043326; AAC09296.1; -.
DR EMBL; BC016526; AAH16526.1; -.
DR HSSP; P30418; INMT.
DR MGD; MGI:102579; Nmt1.
DR InterPro; IPR000903; Nmt.
DR Pfam; PF01233; NMT; 1.
DR PROSITE; PS02799; NMT_C; 1.
DR PROSITE; PS00975; NMT_1; 1.
DR PROSITE; PS00976; NMT_2; 1.
KW Transferase; Acyltransferase.
FT DOMAIN 55 67 POLY-LYS.
SQ SEQUENCE 496 AA; 5688 MW; 61FA7B854A5CF3BC CRC64;
Query Match 29.4%; Score 48; DB 1; Length 496;
Best Local Similarity 24.5%; Pred. No. 29;
Matches 12; Conservative 7; Mismatches 12; Indels 18; Gaps 1;
QY 1 TVOKLAHQIYQFTD-----KDKDNVAPRSKISPOGY 31
Db 108 TMEASKRSYQFWDTPVPKLGWVNHGVEPVDKDNIRQEPYTLPGF 156
|:::|::|
|:::|::|

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Search completed: October 14, 2003, 08:39:11
Job time : 11.8636 secs

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OM protein - protein search, using sw model

Run on: October 14, 2003, 08:36:06 ; Search time 41.5682 Seconds
(without alignments)
192.446 Million cell updates/sec

Title: US-09-931-700-3
Perfect score: 163
Sequence: 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp.archaea:*
- 2: sp.bacteria:*
- 3: sp.fungi:*
- 4: sp.human:*
- 5: sp.invertebrate:*
- 6: sp.mammal:*
- 7: sp.mhc:*
- 8: sp.organelle:*
- 9: sp.phage:*
- 10: sp.plant:*
- 11: sp.podent:*
- 12: sp.virus:*
- 13: sp.vertibrate:*
- 14: sp.unclassified:*
- 15: sp.rvirus:*
- 16: sp.bacteriap:*
- 17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	146	89.6	188	6 Q95KP0	Q95kp0 bos taurus
2	138	84.7	27	6 Q9TRZ6	Q9trz6 sus scrofa
3	58.5	35.9	189	16 Q8XA03	Q8xa03 escherichia
4	58	35.6	430	10 Q23846	Q23846 brassica ol
5	56	34.4	367	10 Q9SEB5	Q9seb5 hirschioidi
6	56	34.4	431	10 Q23849	Q23849 brassica ol
7	55	33.7	368	10 Q9SBP2	Q9sbp2 raphanus ra
8	55	33.7	421	10 Q8S9B2	Q8s9b2 brassica ol
9	54	33.1	373	16 Q9K6R4	Q9k6r4 bacillus ha
10	53	32.5	346	5 Q9BIA5	Q9bia5 caenorhabdi
11	53	32.5	357	5 Q9BIA9	Q9bia9 caenorhabdi
12	53	32.5	430	10 Q8H0C3	Q8h0c3 brassica na
13	52	31.9	428	10 Q23839	Q23839 brassica ol
14	52	31.9	507	12 Q56958	Q56958 human papil
15	52	31.9	775	2 Q8L163	Q8l163 thermoanaer
16	52	31.9	963	11 Q8K0C1	Q8k0c1 mus musculu

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17 52 31.9 1004 2 Q8GHM6
18 51.5 31.6 620 16 Q8G3H2
19 51 31.3 161 2 Q9S412
20 51 31.3 418 10 Q39280
21 51 31.3 428 10 Q80351
22 51 31.3 429 10 Q23843
23 51 31.3 857 10 Q39392
24 51 31.3 859 10 Q9MB87
25 51 31.3 892 5 Q9V3Z4
26 51 31.3 898 5 Q8MSU8
27 50 30.7 90 10 Q9M9R8
28 50 30.7 425 10 Q8S9B0
29 50 30.7 427 10 Q23859
30 50 30.7 428 10 Q23857
31 50 30.7 436 10 Q9SAZ7
32 50 30.7 653 16 Q984T6
33 50 30.7 846 10 Q9ZNW9
34 50 30.7 860 10 Q9ZNM6
35 50 30.7 1181 4 Q96JV0
36 50 30.7 1412 4 Q96JM2
37 49.5 30.4 167 8 Q951T7
38 49.5 30.4 167 8 Q951T9
39 49.5 30.4 167 8 Q94P28
40 49.5 30.4 167 8 Q951U0
41 49.5 30.4 167 8 Q951T8
42 49.5 30.4 227 8 Q958G9
43 49.5 30.4 352 10 Q9LJ66
44 49 30.1 59 17 Q97AP4
45 49 30.1 397 10 Q8LCQ2

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ALIGNMENTS

RESULT 1

Q95KP0 PRELIMINARY; PRT; 188 AA.

AC Q95KP0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Adrenomedullin.
GN PBAM-2.

OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;

RN [1]
RP SEQUENCE FROM N.A.

RA Kitamura K., Matsui E., Kato J., Katoh F., Kita T., Tsuji T.,
RA Kangawa K., Eto T.;

RT "ADRENOMEDULLIN (11-26): AN ENDOGENOUS HYPERTENSIVE PEPTIDE ISOLATED
RT FROM BOVINE ADRENAL MEDULLA.";

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

RL EMBL; AB055107; BAB62176.1; -

DR InterPro; IPR001710; Adrenomedullin.

DR Pfam; PF02039; Adrenomedullin; 1.

DR PRINTS; PR00801; ADRENOMEDULLN.

SQ SEQUENCE 188 AA; 20963 MW; 6102E69A756DCAB6 CRC64;
Query Match 89.6%; Score 146; DB 6; Length 188;
Best Local Similarity 90.3%; Pred. No. 3e-13;

Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 31

Db 116 TVQKLAHQIYHFTDKDKGSAFRSKISPOGY 146

RESULT 2

Q9TRZ6

ID Q9TRZ6 PRELIMINARY; PRT; 27 AA.

RA Luu D.T., Hugues S., Passelegue E., Heizmann P.;
RT "Evidence for orthologous S-locus-related I genes in several genera of

RT Brassicaceae.";
RL Mol. Genet. 264:735-745(2001).
DR EMBL; AF162909; AAF22268.1; -.
DR InterPro; IPR001480; B_lectin.
DR InterPro; IPR000858; Slocus_glycop.
DR Pfam; PF01453; Agglutinin; 1.
DR Pfam; PF00954; S_locus_glycop; 1.
DR SMART; SM00108; B_lectin; 1.
FT NON_TER 1
FT FT 367
SQ SEQUENCE 367 AA; 41676 MW; 48943E2EA85A2E45 CRC64;

Query Match 34.4%; Score 56; DB 10; Length 367;
Best Local Similarity 28.2%; Pred. No. 7.6;
Matches 11; Conservative 9; Mismatches 9; Indels 10; Gaps 1;

QY 3 OKLAHQIQVTFDKD-----NVAPRSKISPGY 31
||||: |||: : : : | | | | |
Db 194 QKLVMYNFENSEEVAYFRMTNNSIYSRLKISSG 232

RESULT 6
O23849 PRELIMINARY; PRT; 431 AA.

ID O23849
AC O23849
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE S glycoprotein (Fragment).
OS Brassica campestris (Field mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3711;
[1]

SEQUENCE FROM N.A.
MEDLINE=97352858; PubMed=9207151;
Kusaba M., Nishio T., Satta Y., Hinata K., Ockendon D.;
"Striking sequence similarity in inter- and intra-specific comparisons
of class I SLG alleles from Brassica oleracea and Brassica
campestris: implications for the evolution and recognition
mechanism."; RT
Proc. Natl. Acad. Sci. U.S.A. 94:7673-7678(1997).
EMBL; D85215; BAA21949.1; -.
DR InterPro; IPR001480; B_lectin.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR000858; Slocus_glycop.
DR Pfam; PF01453; Agglutinin; 1.
DR Pfam; PF00954; S_locus_glycop; 1.
DR SMART; SM00108; B_lectin; 1.
DR SMART; SM00473; PAN_AP; 1.
FT NON_TER 1
FT FT 431
SQ SEQUENCE 431 AA; 49227 MW; BED2FAFB8C3CD4B5 CRC64;

Query Match 34.4%; Score 56; DB 10; Length 431;
Best Local Similarity 30.8%; Pred. No. 9;
Matches 12; Conservative 8; Mismatches 9; Indels 10; Gaps 1;

QY 3 OKLAHQIQVTFDKD-----NVAPRSKISPGY 31
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Db 232 QKLVMYNFENSEEVAYFRMTNNSIYSRLKISSG 270

RESULT 7
Q9SBP2 PRELIMINARY; PRT; 368 AA.

ID Q9SBP2
AC Q9SBP2
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE S-locus related (Fragment).
GN SLR.

OS Raphanus raphanistrum subsp. raphanistrum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Raphanus.
OX NCBI_TaxID=109997;
[1]

SEQUENCE FROM N.A.
RC TISSUE=Pistil;
RA MEDLINE=21148766; PubMed=11254120;
RX Lau D.T., Hugues S., Passeleque E., Heizmann P.;
RT "Evidence for orthologous S-locus-related I genes in several genera of
Brassicaceae."; RL Mol. Genet. 264:735-745(2001).
DR EMBL; AF162905; AAF22264.1; -.
DR InterPro; IPR001480; B_lectin.
DR InterPro; IPR000858; Slocus_glycop.
DR Pfam; PF01453; Agglutinin; 1.
DR Pfam; PF00954; S_locus_glycop; 1.
DR SMART; SM00108; B_lectin; 1.
FT NON_TER 1
FT FT 368
SQ SEQUENCE 368 AA; 41672 MW; ID455F6FB9B704D9 CRC64;

Query Match 33.7%; Score 55; DB 10; Length 368;
Best Local Similarity 28.2%; Pred. No. 11;
Matches 11; Conservative 10; Mismatches 8; Indels 10; Gaps 1;

QY 3 OKLAHQIQVTFDKD-----NVAPRSKISPGY 31
||||: |||: : : : | | | | |
Db 195 QKLVMYNFENSEEVAYFRMTNNSIYSRLKISSG 233

RESULT 8
Q8S9B2 PRELIMINARY; PRT; 421 AA.

ID Q8S9B2
AC Q8S9B2
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE S receptor kinase (Fragment).
GN SRK
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
[1]

SEQUENCE FROM N.A.
RA Kimura R., Sato K., Fujimoto R., Nishio T.;
RT "Recognition specificity of self-incompatibility maintained after the
divergence of Brassica oleracea and Brassica rapa."; RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB070624; BAB86338.1; -.
DR InterPro; IPR001480; B_lectin.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR000858; Slocus_glycop.
DR Pfam; PF01453; Agglutinin; 1.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00954; S_locus_glycop; 1.
DR SMART; SM00108; B_lectin; 1.
DR SMART; SM00473; PAN_AP; 1.
DR Receptor; Kinase.
FT NON_TER 1
FT FT 421
SQ SEQUENCE 421 AA; 48015 MW; 835E29608FC9F160 CRC64;

Query Match 33.7%; Score 55; DB 10; Length 421;
Best Local Similarity 30.8%; Pred. No. 12;
Matches 12; Conservative 8; Mismatches 9; Indels 10; Gaps 1;

QY 3 OKLAHQIQVTFDKD-----NVAPRSKISPGY 31
||||: |||: : : : | | | | |

RT Brassicaceae.";
RL Mol. Genet. 264:735-745(2001).
DR EMBL; AF162909; AAF22268.1; -.
DR InterPro; IPR001480; B_lectin.
DR InterPro; IPR000858; Slocus_glycop.
DR Pfam; PF01453; Agglutinin; 1.
DR Pfam; PF00954; S_locus_glycop; 1.
DR SMART; SM00108; B_lectin; 1.
FT NON_TER 1
FT FT 367
SQ SEQUENCE 367 AA; 41676 MW; 48943E2EA85A2E45 CRC64;

Query Match 34.4%; Score 56; DB 10; Length 367;
Best Local Similarity 28.2%; Pred. No. 7.6;
Matches 11; Conservative 9; Mismatches 9; Indels 10; Gaps 1;

QY 3 OKLAHQIYQFTDKD-----NVAPRSKISPGY 31
||||: |||: : : : | | | |
Db 194 QKLVMYNFENSEEVAYFRMTNNSIYSRLKISSG 232

RESULT 6
ID O23849 PRELIMINARY; PRT; 431 AA.
AC O23849;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE S glycoprotein (Fragment).
OS Brassica campestris (Field mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3711;
[1]

SEQUENCE FROM N.A.
MEDLINE=97352858; PubMed=9207151;
Kusaba M., Nishio T., Satta Y., Hinata K., Ockendon D.;
"Striking sequence similarity in inter- and intra-specific comparisons
of class I SLG alleles from Brassica oleracea and Brassica
campestris: implications for the evolution and recognition
mechanism."; RT
Proc. Natl. Acad. Sci. U.S.A. 94:7673-7678(1997).
EMBL; D85215; BAA21949.1; -.
DR InterPro; IPR001480; B_lectin.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR000858; Slocus_glycop.
DR Pfam; PF01453; Agglutinin; 1.
DR Pfam; PF00954; S_locus_glycop; 1.
DR SMART; SM00108; B_lectin; 1.
DR SMART; SM00473; PAN_AP; 1.
FT NON_TER 1
FT FT 431
SQ SEQUENCE 431 AA; 49227 MW; BED2FAFB8C3CD4B5 CRC64;

Query Match 34.4%; Score 56; DB 10; Length 431;
Best Local Similarity 30.8%; Pred. No. 9;
Matches 12; Conservative 8; Mismatches 9; Indels 10; Gaps 1;

QY 3 OKLAHQIYQFTDKD-----NVAPRSKISPGY 31
||||: |||: : : : | | | |
Db 232 QKLVMYNFENSEEVAYFRMTNNSIYSRLKISSG 270

RESULT 7
ID Q9SBP2 PRELIMINARY; PRT; 368 AA.
AC Q9SBP2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE S-locus related (Fragment).
GN SLR.

OS Raphanus raphanistrum subsp. raphanistrum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Raphanus.
OX NCBI_TaxID=109997;
[1]

SEQUENCE FROM N.A.
RC TISSUE=Pistil;
RA MEDLINE=21148766; PubMed=11254120;
RX Lau D.T., Hugues S., Passeleque E., Heizmann P.;
RT "Evidence for orthologous S-locus-related I genes in several genera of
Brassicaceae."; RL Mol. Genet. 264:735-745(2001).
DR EMBL; AF162905; AAF22264.1; -.
DR InterPro; IPR001480; B_lectin.
DR InterPro; IPR000858; Slocus_glycop.
DR Pfam; PF01453; Agglutinin; 1.
DR Pfam; PF00954; S_locus_glycop; 1.
DR SMART; SM00108; B_lectin; 1.
FT NON_TER 1
FT FT 368
SQ SEQUENCE 368 AA; 41672 MW; ID455F6FB9B704D9 CRC64;

Query Match 33.7%; Score 55; DB 10; Length 368;
Best Local Similarity 28.2%; Pred. No. 11;
Matches 11; Conservative 10; Mismatches 8; Indels 10; Gaps 1;

QY 3 OKLAHQIYQFTDKD-----NVAPRSKISPGY 31
||||: |||: : : : | | | |
Db 195 QKLVMYNFENSEEVAYFRMTNNSIYSRLKISSG 233

RESULT 8
ID Q8S9B2 PRELIMINARY; PRT; 421 AA.
AC Q8S9B2;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE S receptor kinase (Fragment).
GN SRK
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
[1]

SEQUENCE FROM N.A.
RA Kimura R., Sato K., Fujimoto R., Nishio T.;
RT "Recognition specificity of self-incompatibility maintained after the
divergence of Brassica oleracea and Brassica rapa."; RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB070624; BAB86338.1; -.
DR InterPro; IPR001480; B_lectin.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR000858; Slocus_glycop.
DR Pfam; PF01453; Agglutinin; 1.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00954; S_locus_glycop; 1.
DR SMART; SM00108; B_lectin; 1.
DR SMART; SM00473; PAN_AP; 1.
DR Receptor; Kinase.
FT NON_TER 1
FT FT 421
SQ SEQUENCE 421 AA; 48015 MW; 835E29608FC9F160 CRC64;

Query Match 33.7%; Score 55; DB 10; Length 421;
Best Local Similarity 30.8%; Pred. No. 12;
Matches 12; Conservative 8; Mismatches 9; Indels 10; Gaps 1;

QY 3 OKLAHQIYQFTDKD-----NVAPRSKISPGY 31
||||: |||: : : : | | | |

Db 227 QKLSYMYNFTDNSEVAYFTLMTNNSFYSRLKLSSEGY 265

RESULT 9

Q9K6R4
ID Q9K6R4 PRELIMINARY; PRT; 373 AA.
AC Q9K6R4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Lipopolysaccharide biosynthesis.
GN BH3663.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirana C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
RA "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001519; BAB07382.1; -.
DR InterPro; IPR001296; Glyco_transf_1.
DR Pfam; PF00534; Glycos_transf_1; 1.
KW Complete proteome.
SQ SEQUENCE 373 AA; 42062 MW; 0C67C2C98CBA4107 CRC64;

Query Match 33.1%; Score 54; DB 16; Length 373;
Best Local Similarity 48.0%; Pred. No. 15;
Matches 12; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 2 VOKLAHQIYQFTDKDKDNVAPRSKI 26

Db 132 VYKLAHQIYSLSEGVKENLVRYKI 156

RESULT 10

Q9BIA5
ID Q9BIA5 PRELIMINARY; PRT; 346 AA.
AC Q9BIA5;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical 39.7 kDa protein.
GN C17C3.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RA "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RA "Direct Submission.";
RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; U41279; AAK31428.1; -.
DR EMBL; U41279; AAK31428.1; -.
DR HSSP; P23911; 1C8U.
DR WormPep; C17C3.1a; CE27070.
DR InterPro; IPR003703; Acyl_CoA_thio.
DR Pfam; PF02551; Acyl_CoA_thio; 2.
DR TIGRFAMs; TIGR00189; tesB; 1.
KW Hypothetical protein.
SQ SEQUENCE 357 AA; 41046 MW; D62561FC872C1158 CRC64;

Query Match 32.5%; Score 53; DB 5; Length 357;
Best Local Similarity 40.0%; Pred. No. 20;
Matches 8; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 3 OKLAHQIYQFTDKDKDNVAP 22

Db 48 QEIAHKFFDTLKKDSFSP 67

RESULT 12

Q8HOC3
ID Q8HOC3 PRELIMINARY; PRT; 430 AA.
AC Q8HOC3;

DR EMBL; U41279; AAK31429.1; -.
DR HSSP; P23911; 1C8U.
DR WormPep; C17C3.1b; CE27071.
DR InterPro; IPR003703; Acyl_CoA_thio.
DR Pfam; PF02551; Acyl_CoA_thio; 2.
DR TIGRFAMs; TIGR00189; tesB; 1.
KW Hypothetical protein.
SQ SEQUENCE 346 AA; 39688 MW; CF853F9CAF0B93B2 CRC64;

Query Match 32.5%; Score 53; DB 5; Length 346;
Best Local Similarity 40.0%; Pred. No. 19;
Matches 8; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 3 OKLAHQIYQFTDKDKDNVAP 22

Db 37 QEIAHKFFDTLKKDSFSP 56

RESULT 11

Q9BIA9
ID Q9BIA9 PRELIMINARY; PRT; 357 AA.
AC Q9BIA9;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical 41.0 kDa protein.
GN C17C3.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RA "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Du Z.;
RA "The sequence of C. elegans cosmid C17C3.";
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Waterston R.;
RA "Direct Submission.";
RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; U41279; AAK31428.1; -.
DR EMBL; U41279; AAK31428.1; -.
DR HSSP; P23911; 1C8U.
DR WormPep; C17C3.1a; CE27070.
DR InterPro; IPR003703; Acyl_CoA_thio.
DR Pfam; PF02551; Acyl_CoA_thio; 2.
DR TIGRFAMs; TIGR00189; tesB; 1.
KW Hypothetical protein.
SQ SEQUENCE 357 AA; 41046 MW; D62561FC872C1158 CRC64;

Query Match 32.5%; Score 53; DB 5; Length 357;
Best Local Similarity 40.0%; Pred. No. 20;
Matches 8; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 3 OKLAHQIYQFTDKDKDNVAP 22

Db 48 QEIAHKFFDTLKKDSFSP 67

RESULT 12

Q8HOC3
ID Q8HOC3 PRELIMINARY; PRT; 430 AA.
AC Q8HOC3;

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DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE S-locus glycoprotein (Fragment).
GN SLG.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RA Odashima M., Okamoto S., Nishio T.;
RL "Distribution of S haplotypes in Brassica napus.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AB086974; BAC53782.1; -
FT NON_TER 1 430
FT NON_TER 430 430
SQ SEQUENCE 430 AA; 49065 MW; 60152ED337CD0928 CRC64;

Query Match 32.5%; Score 53; DB 10; Length 430;
Best Local Similarity 25.6%; Pred. No. 25;
Matches 10; Conservative 10; Mismatches 9; Indels 10; Gaps 1;

QY 3 QKLAHQIYQFTDKD-----NVAPRSKISPGY 31
||| : : || : : : : || : :
Db 230 QKLSYVYNFTENSEVAYTFRITNNSIYRLKVSSEGF 268

RESULT 13
O23839
ID O23839 PRELIMINARY; PRT; 428 AA.
AC O23839;
DT 01-JAN-1998 (TremBLrel. 05, Created)
DT 01-JAN-1998 (TremBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE S glycoprotein (Fragment).
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
RN [1]
RP SEQUENCE FROM N.A.
RA Kusaba M., Nishio T., Satta Y., Hinata K., Ockendon D.;
RL "Striking sequence similarity in inter- and intra-specific comparisons
of class I SLG alleles from Brassica oleracea and Brassica
campestris: Implications for the evolution and recognition
mechanism.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:7673-7678(1997).
DR EMBL: D85205; BAA21939.1; -.
DR InterPro: IPR001480; B_lectin.
DR InterPro: IPR003609; Pan_app.
DR InterPro: IPR000858; Slocus_glycop.
DR Pfam: PF01453; Agglutinin; 1.
DR Pfam: PF00954; S_lectin; 1.
DR SMART: SM00108; B_lectin; 1.
DR SMART: SM00473; PAN_AP; 1.
FT NON_TER 1 428
FT NON_TER 428 428
SQ SEQUENCE 428 AA; 48724 MW; 18E04542C7293BEA CRC64;

Query Match 31.9%; Score 52; DB 10; Length 428;
Best Local Similarity 28.2%; Pred. No. 34;
Matches 11; Conservative 8; Mismatches 10; Indels 10; Gaps 1;

QY 3 QKLAHQIYQFTDKD-----NVAPRSKISPGY 31
||| : : || : : : : || : :
Db 229 QKLSYVYNFTENSEVAYTFRITNNSIYRLKVSSEGF 267

RESULT 14

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O56958
ID O56958 PRELIMINARY; PRT; 507 AA.
AC O56958;
DT 01-JUN-1998 (TremBLrel. 06, Created)
DT 01-JUN-1998 (TremBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TremBLrel. 17, Last annotation update)
DE E6, E7, E1, E2, E4, E12, and L1 genes.
GN L1.
OS Human papillomavirus type 80.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=69987;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98118461; PubMed=9454709;
RA Bellus H., Saegling B., Bergmann K., Shananin V., de Villiers E.M.;
RL "The genomes of three of four novel HPV types, defined by differences
of their L1 genes, show high conservation of the E7 gene and the
UTR.";
RL Virology 240:359-365(1998).
DR EMBL: Y15176; CAA75476.1; -.
DR InterPro: IPR002210; PV_capsid_L1.
DR Pfam: PF00500; late_protein_L1; 1.
DR PRINTS: PR00865; HPV_CAPSID_L1.
DR ProDom: PD000544; PV_capsid_L1; 1.
SQ SEQUENCE 507 AA; 56998 MW; 6F17589CC91004F6 CRC64;

Query Match 31.9%; Score 52; DB 12; Length 507;
Best Local Similarity 38.2%; Pred. No. 41;
Matches 13; Conservative 3; Mismatches 14; Indels 4; Gaps 1;

QY 1 TVQKLAHQIYQFTD----KDKDNVAPRSKISPG 30
| | | : | | | : | | | : |
Db 420 TPDNAVHDIYRIDSKATKCPDAVPKDKEDPFG 453

RESULT 15
O8L163
ID O8L163 PRELIMINARY; PRT; 775 AA.
AC O8L163;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Kojibiose phosphorylase.
GN KOJP.
OS Thermoanaerobacter brockii (Thermoanaerobium brockii).
OC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
OC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=29323;
RN [1]
RP SEQUENCE FROM N.A.
RA Maruta K., Mukai K., Kubota M., Chaen H., Fukuda S., Kurimoto M.;
RL "The genes encoding a trehalose phosphorylase and a kojibiose
phosphorylase from Thermoanaerobacter brockii ATCC35047.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AB073931; BAB97300.1; -.
DR InterPro: IPR005194; Glyco_hydro_65C.
DR InterPro: IPR005195; Glyco_hydro_65M.
DR InterPro: IPR005196; Glyco_hydro_65N.
DR Pfam: PF03633; Glyco_hydro_65C; 1.
DR Pfam: PF03632; Glyco_hydro_65M; 1.
DR Pfam: PF03636; Glyco_hydro_65N; 1.
SQ SEQUENCE 775 AA; 89700 MW; FB9760F02B220E56 CRC64;

Query Match 31.9%; Score 52; DB 2; Length 775;
Best Local Similarity 36.0%; Pred. No. 65;
Matches 9; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 6 AHQIYQFTDKDNVAPRSKISPG 30
| : : : | : : : | : :
Db 217 AVRLHYEDKEKNNAIKFRFLPLG 241

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Search completed: October 14, 2003, 08:40:19
Job time : 44.5682 secs

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OM protein - protein search, using sw model

Run on: October 14, 2003, 08:37:31 ; Search time 20.4318 Seconds
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64.196 Million cell updates/sec

Title: US-09-931-700-3
Perfect score: 163
Sequence: 1 TVOKLAHQIYQFTDKDNVAPRSKISPOGY 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	163	100.0	31	3 US-09-070-504-23	Sequence 23, Appl
2	163	100.0	31	4 US-09-011-922A-3	Sequence 3, Appl
3	163	100.0	31	4 US-09-011-922A-14	Sequence 14, Appl
4	163	100.0	31	4 US-09-280-501-9	Sequence 9, Appl
5	163	100.0	38	4 US-09-280-501-6	Sequence 6, Appl
6	163	100.0	40	4 US-09-280-501-11	Sequence 11, Appl
7	163	100.0	52	3 US-09-070-504-14	Sequence 14, Appl
8	163	100.0	185	1 US-08-233-389C-1	Sequence 1, Appl
9	163	100.0	185	2 US-08-801-863-1	Sequence 1, Appl
10	163	100.0	185	2 US-08-486-596A-1	Sequence 1, Appl
11	163	100.0	185	4 US-09-004-713-1	Sequence 1, Appl
12	158	96.9	30	4 US-09-280-501-5	Sequence 5, Appl
13	157	96.3	188	1 US-08-233-389C-3	Sequence 3, Appl
14	157	96.3	188	2 US-08-801-863-3	Sequence 3, Appl
15	157	96.3	188	2 US-08-486-596A-3	Sequence 3, Appl
16	157	96.3	188	2 US-09-004-713-3	Sequence 3, Appl
17	154	94.5	29	4 US-09-280-501-4	Sequence 4, Appl
18	150	92.0	40	4 US-09-280-501-8	Sequence 8, Appl
19	150	92.0	50	4 US-09-280-501-7	Sequence 7, Appl
20	149	91.4	28	4 US-09-280-501-3	Sequence 3, Appl
21	146	90.8	50	3 US-09-070-504-15	Sequence 15, Appl
22	144	88.3	27	4 US-09-280-501-2	Sequence 2, Appl
23	140	85.9	26	4 US-09-280-501-1	Sequence 1, Appl
24	123	75.5	23	4 US-09-280-501-17	Sequence 17, Appl
25	112	68.7	21	4 US-09-280-501-16	Sequence 16, Appl
26	74	45.4	13	4 US-09-280-501-15	Sequence 15, Appl
27	68	41.7	13	4 US-09-280-501-10	Sequence 10, Appl

28 57 35.0 13 4 US-09-011-922A-2 Sequence 2, Appl
29 52 31.9 775 3 US-08-966-388-4 Sequence 4, Appl
30 52 31.9 775 3 US-09-188-403-4 Sequence 4, Appl
31 52 31.9 775 3 US-09-188-404-4 Sequence 4, Appl
32 52 31.9 775 3 US-09-281-259-4 Sequence 4, Appl
33 52 31.9 1005 4 US-09-252-991A-24655 Sequence 24655, A
34 51 31.3 10 2 US-08-934-222-17 Sequence 17, Appl
35 51 31.3 10 2 US-08-933-402-17 Sequence 17, Appl
36 51 31.3 10 2 US-09-207-621-17 Sequence 17, Appl
37 51 31.3 10 2 US-08-532-818-17 Sequence 17, Appl
38 51 31.3 10 3 US-09-231-797-17 Sequence 17, Appl
39 51 31.3 10 3 US-08-934-224-17 Sequence 17, Appl
40 51 31.3 10 3 US-08-933-843-17 Sequence 17, Appl
41 51 31.3 10 3 US-08-934-223-17 Sequence 17, Appl
42 51 31.3 10 3 US-09-413-492-17 Sequence 17, Appl
43 50 30.7 9 4 US-09-280-501-14 Sequence 14, Appl
44 48 29.4 478 4 US-09-786-240-31 Sequence 31, Appl
45 47 28.8 858 2 US-08-265-628-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-070-504-23
; Sequence 23, Application US/09070504
; Patent No. 6268474
; GENERAL INFORMATION:
; APPLICANT: Smith, Derek D.
; APPLICANT: Saha, Shankar
; APPLICANT: Abel, Peter W.
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
; TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muetting, Raasch & Gebhardt, P.A.
; STREET: 119 No. 6268474th Fourth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,504
; FILING DATE: 30-APR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 180.00020101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/305-1220
; TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: Single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-070-504-23

Query Match 100.0%; Score 163; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.4e-19;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TVOKLAHQIYQFTDKDNVAPRSKISPOGY 31
Db 1 TVOKLAHQIYQFTDKDNVAPRSKISPOGY 31

RESULT 2
US-09-011-922A-3
; Sequence 3, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
; APPLICANT: Cuttitta, Frank; Martinez,
; APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
; APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
; APPLICANT: Karen; Macri, Charles
; TITLE OF INVENTION: Functional Role of
; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
; TITLE OF INVENTION: Product (PAMP) in Human Pathology and
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS WORD 97
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011.922A
; FILING DATE: 17-Feb-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002.514
; FILING DATE: 18-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002.936
; FILING DATE: 30-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/013.172
; FILING DATE: 12-Mar-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13286
; FILING DATE: 16-Aug-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Leslie A. Serunian
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4202US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: P072
; OTHER INFORMATION: PreproAM(116-146)
US-09-011-922A-3

Query Match 100.0%; Score 163; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.4e-19;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31

RESULT 3
US-09-011-922A-14

; Sequence 14, Application US/09011922A
; Patent No. 6320022
; GENERAL INFORMATION:
; APPLICANT: Cuttitta, Frank; Martinez,
; APPLICANT: Alfredo; Miller, Mae Jean; Unsworth, Edward
; APPLICANT: J.; Hook, William; Walsh, Thomas; Grey,
; APPLICANT: Karen; Macri, Charles
; TITLE OF INVENTION: Functional Role of
; TITLE OF INVENTION: Adrenomedullin (AM) and the Gene-Related
; TITLE OF INVENTION: Product (PAMP) in Human Pathology and
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS WORD 97
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/011.922A
; FILING DATE: 17-Feb-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002.514
; FILING DATE: 18-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/002.936
; FILING DATE: 30-Aug-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/60/013.172
; FILING DATE: 12-Mar-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13286
; FILING DATE: 16-Aug-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Leslie A. Serunian
; REGISTRATION NUMBER: 35,353
; REFERENCE/DOCKET NUMBER: 2026-4202US3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; OTHER INFORMATION: Synthetic homolog of
; OTHER INFORMATION: two-thirds of the intact AM peptide
US-09-011-922A-14

Query Match 100.0%; Score 163; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.4e-19;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
DB 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31

RESULT 4
US-09-280-501-9
; Sequence 9, Application US/09280501
; Patent No. 6440421
; GENERAL INFORMATION:
; APPLICANT: Cooper, Garth James Smith


```
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,389C
; FILING DATE: 26-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-233-389C-1

Query Match 100.0%; Score 163; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 2,1e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 31
Db 116 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 146

RESULT 9
US-08-801-863-1
; Sequence 1, Application US/08801863
; Patent No. 5830703
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,863
; FILING DATE: CONCURRENTLY HEREWITH
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; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-801-863-1

Query Match 100.0%; Score 163; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 2,1e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 31
Db 116 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 146

RESULT 10
US-08-486-596A-1
; Sequence 1, Application US/08486596A
; Patent No. 5837823
; GENERAL INFORMATION:
; APPLICANT: KITAMURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,596A
; FILING DATE: JUNE 7, 1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY Jr., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5 DIV1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-486-596A-1

Query Match 100.0%; Score 163; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 2,1e-18;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 31
Db 116 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 146
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Db 116 TVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 146

RESULT 11

US-09-004-713-1
 ; Sequence 1, Application US/09004713
 ; Patent No. 5910416
 ; GENERAL INFORMATION:
 ; APPLICANT: KITAMURA, Kazuo
 ; APPLICANT: KANGAWA, Kenji
 ; APPLICANT: MATSUO, Hisayuki
 ; APPLICANT: ETO, Tanenao
 ; TITLE OF INVENTION: ADRENOMEDULLIN
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: c/o FISH & NEAVE
 ; STREET: 1251 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10020
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION NUMBER: US/09/004,713
 ; FILING DATE: JANUARY 7, 1998
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: HALEY Jr., James F.
 ; REGISTRATION NUMBER: 27,794
 ; REFERENCE/DOCKET NUMBER: SHGN-5 DIV2 CON
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 596-9000
 ; TELEFAX: (212) 596-9090
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 185 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-004-713-1

Query Match 100.0%; Score 163; DB 2; Length 185;
 Best Local Similarity 100.0%; Pred. No. 2.1e-18;
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RESULT 12

US-09-280-501-5
 ; Sequence 5, Application US/09280501
 ; Patent No. 6440421
 ; GENERAL INFORMATION:
 ; APPLICANT: Cooper, Garth James Smith
 ; APPLICANT: Reid, Ian Reginald
 ; APPLICANT: Cornish, Jillian
 ; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
 ; FILE REFERENCE: 08987-005001
 ; CURRENT APPLICATION NUMBER: US/09/280,501
 ; CURRENT FILING DATE: 1999-03-30
 ; PRIOR APPLICATION NUMBER: 08/634,562
 ; PRIOR FILING DATE: 1996-04-18
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 30

; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-280-501-5

Query Match 96.9%; Score 158; DB 4; Length 30;
 Best Local Similarity 100.0%; Pred. No. 1.5e-18;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VQKLAHQIYQFTDKDKDNVAPRSKISPOGY 31
 Db 1 VQKLAHQIYQFTDKDKDNVAPRSKISPOGY 30

RESULT 13

US-08-233-389C-3
 ; Sequence 3, Application US/08233389C
 ; Patent No. 5639855
 ; GENERAL INFORMATION:
 ; APPLICANT: KITAMURA, Kazuo
 ; APPLICANT: KANGAWA, Kenji
 ; APPLICANT: MATSUO, Hisayuki
 ; APPLICANT: ETO, Tanenao
 ; TITLE OF INVENTION: ADRENOMEDULLIN
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: c/o FISH & NEAVE
 ; STREET: 1251 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10020
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/233,389C
 ; FILING DATE: 26-APR-1994
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: HALEY Jr., James F.
 ; REGISTRATION NUMBER: 27,794
 ; REFERENCE/DOCKET NUMBER: SHGN-5
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 596-9000
 ; TELEFAX: (212) 596-9090
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 188 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-233-389C-3

Query Match 96.3%; Score 157; DB 1; Length 188;
 Best Local Similarity 96.8%; Pred. No. 2e-17;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Db 116 TVQKLAHQIYQFTDKDKDNVAPRSKISPOGY 146

RESULT 14

US-08-801-863-3
 ; Sequence 3, Application US/08801863
 ; Patent No. 5830703
 ; GENERAL INFORMATION:
 ; APPLICANT: KITAMURA, Kazuo
 ; APPLICANT: KANGAWA, Kenji
 ; APPLICANT: MATSUO, Hisayuki
 ; APPLICANT: ETO, Tanenao


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; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: C/O FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,863
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY JR., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5 DIV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-801-863-3

Query Match          96.3%; Score 157; DB 2; Length 188;
Best Local Similarity 96.8%; Pred. No. 2e-17;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
Db 116 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 146

RESULT 15
US-08-486-596A-3
; Sequence 3, Application US/08486596A
; Patent No. 5837823
; GENERAL INFORMATION:
; APPLICANT: KITAHURA, Kazuo
; APPLICANT: KANGAWA, Kenji
; APPLICANT: MATSUO, Hisayuki
; APPLICANT: ETO, Tanenao
; TITLE OF INVENTION: ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: C/O FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,596A
; FILING DATE: JUNE 7, 1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY JR., James F.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: SHGN-5 DIV1
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-486-596A-3
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Query Match          96.3%; Score 157; DB 2; Length 188;
Best Local Similarity 96.8%; Pred. No. 2e-17;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
Db 116 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 146
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Job time : 21.4318 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 14, 2003, 08:40:27 ; Search time 62 seconds
(without alignments)
80.564 Million cell updates/sec

Title: US-09-931-700-3
Perfect score: 163
Sequence: 1 TVQKLAHQIYQTDKDKDNVAPRSKISPGY 31

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Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	163	100.0	31	9 US-09-931-700-14	Sequence 14, Appl
3	163	100.0	31	9 US-09-813-345-23	Sequence 23, Appl
4	163	100.0	52	9 US-09-813-345-14	Sequence 14, Appl
5	163	100.0	52	15 US-10-197-954-2	Sequence 2, Appli
6	148	90.8	50	9 US-09-813-345-15	Sequence 15, Appl
7	57	35.0	13	9 US-09-931-700-2	Sequence 2, Appli
8	48	29.4	478	12 US-10-427-631-31	Sequence 31, Appl
9	48	29.4	1745	12 US-09-795-061-4	Sequence 4, Appli
10	47.5	29.1	984	15 US-10-128-714-3547	Sequence 3547, Ap
11	47.5	29.1	1058	15 US-10-128-714-8547	Sequence 8547, Ap
12	47	28.8	33	9 US-09-864-761-43882	Sequence 43882, A
13	47	28.8	327	15 US-10-102-806-570	Sequence 570, App
14	46.5	28.5	131	12 US-09-903-190-174	Sequence 174, App
15	46	28.2	608	12 US-09-738-269-41	Sequence 41, Appl

16	46	28.2	608	14	US-10-023-437-41	Sequence 41, Appl
17	45	27.6	211	11	US-09-791-279-219	Sequence 219, App
18	45	27.6	281	12	US-10-269-017-1	Sequence 1, Appli
19	44.5	27.3	293	12	US-10-352-393-5	Sequence 5, Appli
20	44.5	27.3	437	12	US-10-032-585-7130	Sequence 7130, Ap
21	44	27.0	210	12	US-09-882-227-180	Sequence 180, App
22	44	27.0	462	9	US-09-846-729A-3	Sequence 3, Appli
23	44	27.0	462	9	US-09-846-729A-17	Sequence 17, Appli
24	44	27.0	462	12	US-10-441-667-3	Sequence 3, Appli
25	44	27.0	462	12	US-10-441-667-17	Sequence 17, Appli
26	44	27.0	462	9	US-09-846-729A-14	Sequence 14, Appl
27	44	27.0	462	12	US-10-441-667-14	Sequence 14, Appl
28	44	27.0	478	15	US-10-078-866-2	Sequence 2, Appli
29	44	27.0	483	12	US-10-439-533-2	Sequence 2, Appli
30	43.5	26.7	175	12	US-10-216-163-74	Sequence 74, Appl
31	43.5	26.7	175	12	US-10-218-765-74	Sequence 74, Appl
32	43.5	26.7	175	12	US-10-219-066-74	Sequence 74, Appl
33	43.5	26.7	175	12	US-10-219-066-74	Sequence 74, Appl
34	43.5	26.7	175	12	US-10-219-067-74	Sequence 74, Appl
35	43.5	26.7	175	12	US-10-219-068-74	Sequence 74, Appl
36	43.5	26.7	175	12	US-10-219-069-74	Sequence 74, Appl
37	43.5	26.7	175	12	US-10-219-073-74	Sequence 74, Appl
38	43.5	26.7	175	12	US-10-219-475-74	Sequence 74, Appl
39	43.5	26.7	175	12	US-10-219-480-74	Sequence 74, Appl
40	43.5	26.7	175	12	US-10-219-483-74	Sequence 74, Appl
41	43.5	26.7	175	12	US-10-219-525-74	Sequence 74, Appl
42	43.5	26.7	175	12	US-10-219-526-74	Sequence 74, Appl
43	43.5	26.7	175	12	US-10-219-530-74	Sequence 74, Appl
44	43.5	26.7	175	12	US-10-219-531-74	Sequence 74, Appl
45	43.5	26.7	175	12	US-10-219-532-74	Sequence 74, Appl

ALIGNMENTS

RESULT 1
US-09-931-700-3
; Sequence 3, Application US/09931700
; Patent No. US20020055615A1
; GENERAL INFORMATION:
; APPLICANT: CATTUITA, FRANK
; APPLICANT: MARTINEZ, ALFREDO
; APPLICANT: MILLER, MAE JEAN
; APPLICANT: UNSWORTH, EDWARD J.
; APPLICANT: HOOK, WILLIAM
; APPLICANT: WALSH, THOMAS
; APPLICANT: GREY, KAREN
; APPLICANT: MACRI, CHARLES
; TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
; TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; FILE REFERENCE: 2026-4202USA
; CURRENT APPLICATION NUMBER: US/09/931,700
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 09/011,922
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: PCT/US96/13286
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US/60/013,172
; PRIOR FILING DATE: 1996-03-12
; PRIOR APPLICATION NUMBER: US60/002,936
; PRIOR FILING DATE: 1995-08-30
; PRIOR APPLICATION NUMBER: US/60/002,514
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide, P072,
; OTHER INFORMATION: PreproAM (amino acids 116-146)

US-09-931-700-3

Query Match 100.0%; Score 163; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.2e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
|||||
Db 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31

RESULT 2

US-09-931-700-14
; Sequence 14, Application US/09931700
; Patent No. US20020055615A1
; GENERAL INFORMATION:
; APPLICANT: CUTTITTA, FRANK
; APPLICANT: MARTINEZ, ALFREDO
; APPLICANT: MILLER, MAE JEAN
; APPLICANT: UNSWORTH, EDWARD J.
; APPLICANT: HOOK, WILLIAM
; APPLICANT: WALSH, THOMAS
; APPLICANT: GREY, KAREN
; APPLICANT: MACRI, CHARLES
; TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
; TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and
; TITLE OF INVENTION: Physiology
; FILE REFERENCE: 2026-4202US4
; CURRENT APPLICATION NUMBER: US/09/931,700
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 09/011,922
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: PCT/US96/13286
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US/60/013,172
; PRIOR FILING DATE: 1996-03-12
; PRIOR APPLICATION NUMBER: US60/002,936
; PRIOR FILING DATE: 1995-08-30
; PRIOR APPLICATION NUMBER: US/60/002,514
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 14
; LENGTH: 31
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Peptide,
; OTHER INFORMATION: Synthetic homolog of AM (P072), Structural amino
; OTHER INFORMATION: acid sequence representing two-thirds of the
; OTHER INFORMATION: intact AM peptide
US-09-931-700-14

Query Match 100.0%; Score 163; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.2e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
|||||
Db 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31

RESULT 3

US-09-813-345-23
; Sequence 23, Application US/09813345
; Patent No. US20020068814A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Derek D.
; Saha, Shankar
; Abel, Peter W.
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
; SUPERFAMILY AND METHODS OF USE
; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muetting, Raasch & Gebhardt, P.A.
; STREET: 119 No. US20020068814A1th Fourth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,345
; FILING DATE: 20-Mar-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 180.00020101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/305-1220
; TELEFAX: 612/305-1228
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-813-345-23

Query Match 100.0%; Score 163; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.2e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
|||||
Db 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31

RESULT 4
US-09-813-345-14
; Sequence 14, Application US/09813345
; Patent No. US20020068814A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Derek D.
; Saha, Shankar
; Abel, Peter W.
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
; SUPERFAMILY AND METHODS OF USE
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muetting, Raasch & Gebhardt, P.A.
; STREET: 119 No. US20020068814A1th Fourth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,345
; FILING DATE: 20-Mar-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 180.00020101

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612/305-1220

TELEFAX: 612/305-1228

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 52 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-09-813-345-14

Query Match 100.0%; Score 163; DB 9; Length 52;
Best Local Similarity 100.0%; Pred. No. 5.8e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDNVAPRSKISPOGY 31

Db 22 TVQKLAHQIYQFTDKDNVAPRSKISPOGY 52

RESULT 5

US-10-197-954-2

Sequence 2, Application US/10197954

Publication No. US20030119021A1

GENERAL INFORMATION:

APPLICANT: K*ster, Hubert

APPLICANT: Siddiqi, Suhaib

APPLICANT: Little, Daniel

TITLE OF INVENTION: Capture Compounds, Collections Thereof

TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex

TITLE OF INVENTION: Compositions

FILE REFERENCE: 24743-2305

CURRENT APPLICATION NUMBER: US/10/197,954

CURRENT FILING DATE: 2002-07-16

PRIOR APPLICATION NUMBER: 60/306,019

PRIOR FILING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: 60/314,123

PRIOR FILING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: 60/363,433

PRIOR FILING DATE: 2002-03-11

NUMBER OF SEQ ID NOS: 149

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2

LENGTH: 52

TYPE: PRT

ORGANISM: Homo Sapien

US-10-197-954-2

Query Match 100.0%; Score 163; DB 15; Length 52;
Best Local Similarity 100.0%; Pred. No. 5.8e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDNVAPRSKISPOGY 31

Db 22 TVQKLAHQIYQFTDKDNVAPRSKISPOGY 52

RESULT 6

US-09-813-345-15

Sequence 15, Application US/09813345

Patent No. US20020068814A1

GENERAL INFORMATION:

APPLICANT: Smith, Derek D.

Saha, Shankar

Abel, Peter W.

TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESS: Mueting, Raasch & Gebhardt, P.A.

STREET: 119 No. US20020068814A1th Fourth Street

CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,345
FILING DATE: 20-Mar-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: McCormack, Myra H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 180.00020101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
TELEFAX: 612/305-1228
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-813-345-15

Query Match 90.8%; Score 148; DB 9; Length 50;
Best Local Similarity 87.1%; Pred. No. 9.2e-15;
Matches 27; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDNVAPRSKISPOGY 31

Db 20 TVQKLAHQIYQFTDKDNVAPRSKISPOGY 50

RESULT 7

US-09-931-700-2

Sequence 2, Application US/09931700

Patent No. US20020055615A1

GENERAL INFORMATION:

APPLICANT: CUTTITA, FRANK

APPLICANT: MARTINEZ, ALFREDO

APPLICANT: MILLER, MAE JEAN

APPLICANT: UNSWORTH, EDWARD J.

APPLICANT: HOOK, WILLIAM

APPLICANT: WALSH, THOMAS

APPLICANT: GREY, KAREN

APPLICANT: MACRI, CHARLES

TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the

TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and

FILE REFERENCE: 2026-4202US4

CURRENT APPLICATION NUMBER: US/09/931,700

CURRENT FILING DATE: 2001-08-16

PRIOR APPLICATION NUMBER: 09/011,922

PRIOR FILING DATE: 1998-02-17

PRIOR APPLICATION NUMBER: PCT/US96/13286

PRIOR FILING DATE: 1996-08-16

PRIOR APPLICATION NUMBER: US/60/013,172

PRIOR FILING DATE: 1996-03-12

PRIOR APPLICATION NUMBER: US60/002,936

PRIOR FILING DATE: 1995-08-30

PRIOR APPLICATION NUMBER: US/60/002,514

PRIOR FILING DATE: 1995-08-18

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 13

TYPE: PRT

: GENERAL INFORMATION:
 APPLICANT: Greenspan, Daniel S
 APPLICANT: Inamura, Yasutada
 TITLE OF INVENTION: Pro-Alpha 3(V) Collagen Genes
 FILE REFERENCE: 960296 96781
 CURRENT APPLICATION NUMBER: US/09/795,061
 CURRENT FILING DATE: 2001-02-26
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 4

GENERAL INFORMATION: Bo Jiang, Jiang, Bo
APPLICANT: Hu, Wenqi
APPLICANT: Tishkoff, Daniel
APPLICANT: zamudio, Carlos
APPLICANT: Ershkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification
TITLE OF INVENTION: Methods of t
FILE REFERENCE: 10192-018-999
CURRENT APPLICATION NUMBER: US/1
CURRENT FILING DATE: 2002-04-23

```

; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8547
; TYPE: PRT
; LENGTH: 1058
; ORGANISM: Aspergillus fumigatus
US-10-128-714-8547

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Query Match          29.1%; Score 47.5; DB 15; Length 1058;
Best Local Similarity 27.5%; Pred. No. 2.4e+02;
Matches 11; Conservative 10; Mismatches 6; Indels 13; Gaps 1;

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QY      3 QKLAHQIYQFTDK-----DKDNVAPRSKISPG 29
Db      75 QEMVEIFKIDRVNVMVRPKLMLTAVDGVAPKXNQ 114

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RESULT 12
US-09-864-761-43882
; Sequence 43882, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21

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; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43882
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005079.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.77
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.94
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.65
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.69
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.69
; OTHER INFORMATION: EST_HUMAN HIT: AUI40742.1, EVALUATE 1.00e-11
US-09-864-761-43882

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```

Query Match          28.8%; Score 47; DB 9; Length 33;
Best Local Similarity 62.5%; Pred. No. 5.3;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

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QY      2 VQKLAHQIYQFTDK 17
Db      10 VQKLAKENYQFLQTDK 25

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RESULT 13
US-10-102-806-570
; Sequence 570, Application US/10102806
; Publication No. US20030034421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PAL03P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 570
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-102-806-570

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Query Match          28.8%; Score 47; DB 15; Length 327;
Best Local Similarity 41.4%; Pred. No. 73;
Matches 12; Conservative 5; Mismatches 10; Indels 2; Gaps 2;

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QY      4 KLAHQI-YQFTDKDKDNVAPRSKISPGY 31
Db      138 RLEHDVNIQFPDKDDGN-QPQDQITITGY 165

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RESULT 14
US-09-903-190-174
; Sequence 174, Application US/09903190
; Publication No. US20030162176A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Ducleret, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET.021A

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; CURRENT APPLICATION NUMBER: US/09/903,190
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US/09/247,155A
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 174
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -20..-1
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 40,41,43,60,70,76,82,86,105,107
; OTHER INFORMATION: Xaa = any one of the twenty amino acids
US-09-903-190-174

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Query Match      28.5%; Score 46.5; DB 12; Length 131;
Best Local Similarity 33.3%; Pred. No. 30;
Matches 12; Conservative 7; Mismatches 8; Indels 9; Gaps 2;

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QY 2 VOKLAHQ-----IYQFTDKDKDNVAPRSKISPGQY 31
Db 97 IQKLAXQFVXLMLVYETIDK---HLSPDQGYXPXDY 129

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RESULT 15
US-09-738-269-41
; Sequence 41, Application US/09738269
; Publication No. US20030185848A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEMKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTENBOECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
; TITLE OF INVENTION: NUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF
; FILE REFERENCE: UTSD:659
; CURRENT APPLICATION NUMBER: US/09/738,269
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 608
; TYPE: PRT
; ORGANISM: Chlamydia psittaci
US-09-738-269-41

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Query Match      28.2%; Score 46; DB 12; Length 608;
Best Local Similarity 64.3%; Pred. No. 2.1e+02;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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QY 16 KDNVAPRSKISPG 29
Db 6 NKQVPRPRSEISPG 19

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Search completed: October 14, 2003, 08:53:17
Job time : 63 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 14, 2003, 08:38:52 ; Search time 405.114 Seconds
(without alignments)
69.629 Million cell updates/sec

Title: US-09-931-700-3
Perfect score: 163
Sequence: 1 TVQKLAHQIYQFTDKDNVAPRSKISPGQY 31

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main.*
1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep.*
2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
4: /cgn2_6/ptodata/1/paa/US08_COMB.pep.*
5: /cgn2_6/ptodata/1/paa/US081_COMB.pep.*
6: /cgn2_6/ptodata/1/paa/US082_COMB.pep.*
7: /cgn2_6/ptodata/1/paa/US083_COMB.pep.*
8: /cgn2_6/ptodata/1/paa/US084_COMB.pep.*
9: /cgn2_6/ptodata/1/paa/US085_COMB.pep.*
10: /cgn2_6/ptodata/1/paa/US086_COMB.pep.*
11: /cgn2_6/ptodata/1/paa/US087_COMB.pep.*
12: /cgn2_6/ptodata/1/paa/US088_COMB.pep.*
13: /cgn2_6/ptodata/1/paa/US089_COMB.pep.*
14: /cgn2_6/ptodata/1/paa/US090_COMB.pep.*
15: /cgn2_6/ptodata/1/paa/US091_COMB.pep.*
16: /cgn2_6/ptodata/1/paa/US092_COMB.pep.*
17: /cgn2_6/ptodata/1/paa/US093_COMB.pep.*
18: /cgn2_6/ptodata/1/paa/US094_COMB.pep.*
19: /cgn2_6/ptodata/1/paa/US095_COMB.pep.*
20: /cgn2_6/ptodata/1/paa/US096_COMB.pep.*
21: /cgn2_6/ptodata/1/paa/US097A_COMB.pep.*
22: /cgn2_6/ptodata/1/paa/US097B_COMB.pep.*
23: /cgn2_6/ptodata/1/paa/US098_COMB.pep.*
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25: /cgn2_6/ptodata/1/paa/US099B_COMB.pep.*
26: /cgn2_6/ptodata/1/paa/US100_COMB.pep.*
27: /cgn2_6/ptodata/1/paa/US101_COMB.pep.*
28: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
29: /cgn2_6/ptodata/1/paa/US103_COMB.pep.*
30: /cgn2_6/ptodata/1/paa/US104_COMB.pep.*
31: /cgn2_6/ptodata/1/paa/US106_COMB.pep.*
32: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Match	Length	ID	Description
1	163	100.0	31	10	US-08-634-562-9

SUMMARIES

ALIGNMENTS

RESULT 1

US-08-634-562-9
Sequence 9, Application US/08634562
GENERAL INFORMATION:
APPLICANT: Coy, David H.
APPLICANT: Cornish, Jillian
APPLICANT: Reid, Ian Reginald
APPLICANT: Cooper, Garth J.S.
TITLE OF INVENTION: TREATMENT OF BONE DISORDERS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:

2	163	100.0	31	20	US-09-623-548A-938	Sequence 938, App
3	163	100.0	31	20	US-09-657-276-938	Sequence 938, App
4	163	100.0	31	23	US-09-813-345-23	Sequence 23, Appl
5	163	100.0	31	24	US-09-931-700-3	Sequence 3, Appl
6	163	100.0	31	24	US-09-931-700-14	Sequence 14, Appl
7	163	100.0	38	10	US-08-634-562-6	Sequence 6, Appl
8	163	100.0	40	10	US-08-634-562-11	Sequence 11, Appl
9	163	100.0	52	1	PCT-US02-22821-2	Sequence 2, Appl
10	163	100.0	52	20	US-09-623-548A-935	Sequence 935, App
11	163	100.0	52	20	US-09-657-276-935	Sequence 935, App
12	163	100.0	52	23	US-09-813-345-14	Sequence 14, Appl
13	163	100.0	52	27	US-10-197-954-2	Sequence 2, Appl
14	163	100.0	52	29	US-10-360-101-7A	Sequence 7A, Appl
15	163	100.0	113	21	US-09-724-676-63615	Sequence 63615, A
16	163	100.0	113	21	US-09-724-676A-63615	Sequence 63615, A
17	163	100.0	113	32	US-60-453-050-12481	Sequence 12481, A
18	163	100.0	113	32	US-60-453-135-12481	Sequence 12481, A
19	163	100.0	113	32	US-60-466-412-12481	Sequence 12481, A
20	163	100.0	138	32	US-60-453-050-12483	Sequence 12483, A
21	163	100.0	138	32	US-60-453-135-12483	Sequence 12483, A
22	163	100.0	138	32	US-60-466-412-12483	Sequence 12483, A
23	163	100.0	185	8	US-08-484-738A-1	Sequence 1, Appl
24	163	100.0	185	26	US-10-018-924-2	Sequence 2, Appl
25	163	100.0	185	26	US-10-030-298-2	Sequence 2, Appl
26	163	100.0	185	29	US-10-364-889-6	Sequence 6, Appl
27	163	100.0	185	32	US-60-440-088-148	Sequence 148, App
28	163	100.0	185	32	US-60-453-050-12482	Sequence 12482, A
29	163	100.0	185	32	US-60-453-135-12482	Sequence 12482, A
30	163	100.0	185	32	US-60-466-412-12482	Sequence 12482, A
31	163	100.0	185	32	US-60-469-757-148	Sequence 148, App
32	158	96.9	193	28	US-10-206-021-406	Sequence 406, App
33	157	96.3	30	10	US-08-634-562-5	Sequence 5, Appl
34	157	96.3	188	8	US-08-484-738A-3	Sequence 3, Appl
35	157	96.3	188	26	US-10-018-924-4	Sequence 4, Appl
36	157	96.3	188	26	US-10-030-298-4	Sequence 4, Appl
37	154	94.5	29	10	US-08-634-562-4	Sequence 4, Appl
38	150	92.0	36	18	US-09-475-158-31	Sequence 31, Appl
39	150	92.0	36	18	US-09-475-158A-31	Sequence 31, Appl
40	150	92.0	40	10	US-08-634-562-8	Sequence 8, Appl
41	150	92.0	50	10	US-08-634-562-7	Sequence 7, Appl
42	149	91.4	28	10	US-08-634-562-3	Sequence 3, Appl
43	148	90.8	40	20	US-09-623-548A-944	Sequence 944, App
44	148	90.8	40	20	US-09-657-276-944	Sequence 944, App
45	148	90.8	50	23	US-09-813-345-15	Sequence 15, Appl

;; APPLICATION NUMBER: US/08/634,562
;; FILING DATE: 18-APR-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: TSOO, Y. ROCKY
;; REGISTRATION NUMBER: 34,053
;; REFERENCE/DOCKET NUMBER: 08987/002001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/542-5070
;; TELEFAX: 617/542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 31 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-634-562-9

Query Match 100.0%; Score 163; DB 10; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVOKLAHQIYQTDKDKDNVAPRSKISPGY 31
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Db 1 TVOKLAHQIYQTDKDKDNVAPRSKISPGY 31

RESULT 2

US-09-623-548A-938
;; Sequence 938, Application US/09623548A
;; GENERAL INFORMATION:

;; APPLICANT: Conjuchem, Inc.
;; APPLICANT: Bridon, Dominique
;; APPLICANT: Ezrin, Alan
;; APPLICANT: Milner, Peter
;; APPLICANT: Holmes, Darren
;; APPLICANT: Thibaudeau, Karen
;; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
;; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
;; FILE REFERENCE: 2110
;; CURRENT APPLICATION NUMBER: US/09/623,548A
;; CURRENT FILING DATE: 2000-09-05
;; PRIOR APPLICATION NUMBER: 60/134,406
;; PRIOR FILING DATE: 1999-05-17
;; PRIOR APPLICATION NUMBER: 60/153,406
;; PRIOR FILING DATE: 1999-09-10
;; PRIOR APPLICATION NUMBER: 60/159,783
;; PRIOR FILING DATE: 1999-10-18
;; NUMBER OF SEQ ID NOS: 1617
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 938
;; LENGTH: 31
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: Peptide

US-09-623-548A-938

Query Match 100.0%; Score 163; DB 20; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVOKLAHQIYQTDKDKDNVAPRSKISPGY 31
|||||
Db 1 TVOKLAHQIYQTDKDKDNVAPRSKISPGY 31

RESULT 3

US-09-657-276-938
;; Sequence 938, Application US/09657276
;; GENERAL INFORMATION:

;; APPLICANT: Conjuchem, Inc.
;; APPLICANT: Bridon, Dominique
;; APPLICANT: Ezrin, Alan
;; APPLICANT: Milner, Peter
;; APPLICANT: Holmes, Darren
;; APPLICANT: Thibaudeau, Karen
;; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
;; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
;; TITLE OF INVENTION: COMPONENTS
;; FILE REFERENCE: 2110
;; CURRENT APPLICATION NUMBER: US/09/657,276
;; CURRENT FILING DATE: 2000-09-07
;; PRIOR APPLICATION NUMBER: 60/134,406
;; PRIOR FILING DATE: 1999-05-17
;; PRIOR APPLICATION NUMBER: 60/153,406
;; PRIOR FILING DATE: 1999-09-10
;; PRIOR APPLICATION NUMBER: 60/159,783
;; PRIOR FILING DATE: 1999-10-18
;; NUMBER OF SEQ ID NOS: 1617
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 938
;; LENGTH: 31
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: Peptide

US-09-657-276-938

Query Match 100.0%; Score 163; DB 20; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVOKLAHQIYQTDKDKDNVAPRSKISPGY 31
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Db 1 TVOKLAHQIYQTDKDKDNVAPRSKISPGY 31

RESULT 4

US-09-813-345-23
;; Sequence 23, Application US/09813345
;; GENERAL INFORMATION:

;; APPLICANT: Smith, Derek D.
;; Saba, Shankar
;; Abel, Peter W.

;; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
;; SUPERFAMILY AND METHODS OF USE
;; NUMBER OF SEQUENCES: 23
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Muetling, Raasch & Gebhardt, P.A.
;; STREET: 119 North Fourth Street
;; CITY: Minneapolis
;; STATE: MN
;; COUNTRY: USA
;; ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/813,345
FILING DATE: 20-Mar-2001
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: McCormack, Myra H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 180.00020101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220

TELEFAX: 612/305-1228
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Query Match 100.0%; Score 163; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDNVAPRSKISPGY 31
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Db 1 TVQKLAHQIYQFTDKDNVAPRSKISPGY 31

RESULT 5

US-09-931-700-3
Sequence 3, Application US/09931700

GENERAL INFORMATION:
APPLICANT: CUTTITTA, FRANK
APPLICANT: MARTINEZ, ALFREDO
APPLICANT: MILLER, MAE JEAN
APPLICANT: UNSWORTH, EDWARD J.
APPLICANT: HOOK, WILLIAM
APPLICANT: WALSH, THOMAS
APPLICANT: GREY, KAREN
APPLICANT: MACRI, CHARLES

TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physiology
FILE REFERENCE: 2026-4202US4

CURRENT APPLICATION NUMBER: US/09/931,700
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 09/011,922
PRIOR FILING DATE: 1998-02-17
PRIOR APPLICATION NUMBER: PCT/US96/13286
PRIOR FILING DATE: 1996-08-16
PRIOR APPLICATION NUMBER: US/60/013,172
PRIOR FILING DATE: 1996-03-12
PRIOR APPLICATION NUMBER: US60/002,936
PRIOR FILING DATE: 1995-08-30
PRIOR APPLICATION NUMBER: US/60/002,514
PRIOR FILING DATE: 1995-08-18
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide, P072,
OTHER INFORMATION: PreproAM (amino acids 116-146)

US-09-931-700-3

Query Match 100.0%; Score 163; DB 24; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDNVAPRSKISPGY 31
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Db 1 TVQKLAHQIYQFTDKDNVAPRSKISPGY 31

RESULT 6

US-09-931-700-14
Sequence 14, Application US/09931700

GENERAL INFORMATION:
APPLICANT: CUTTITTA, FRANK

APPLICANT: MARTINEZ, ALFREDO
APPLICANT: MILLER, MAE JEAN
APPLICANT: UNSWORTH, EDWARD J.
APPLICANT: HOOK, WILLIAM
APPLICANT: WALSH, THOMAS
APPLICANT: GREY, KAREN
APPLICANT: MACRI, CHARLES
TITLE OF INVENTION: Functional Role of Adrenomedullin (AM) and the
TITLE OF INVENTION: Gene-Related Product (PAMP) in Human Pathology and
TITLE OF INVENTION: Physiology
FILE REFERENCE: 2026-4202US4
CURRENT APPLICATION NUMBER: US/09/931,700
CURRENT FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 09/011,922
PRIOR FILING DATE: 1998-02-17
PRIOR APPLICATION NUMBER: PCT/US96/13286
PRIOR FILING DATE: 1996-08-16
PRIOR APPLICATION NUMBER: US/60/013,172
PRIOR FILING DATE: 1996-03-12
PRIOR APPLICATION NUMBER: US60/002,936
PRIOR FILING DATE: 1995-08-30
PRIOR APPLICATION NUMBER: US/60/002,514
PRIOR FILING DATE: 1995-08-18
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Peptide,

OTHER INFORMATION: Synthetic homology of AM (P072), Structural amino
OTHER INFORMATION: acid sequence representing two-thirds of the
OTHER INFORMATION: intact AM peptide
US-09-931-700-14

Query Match 100.0%; Score 163; DB 24; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.3e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDNVAPRSKISPGY 31
|||||
Db 1 TVQKLAHQIYQFTDKDNVAPRSKISPGY 31

RESULT 7

US-08-634-562-6

Sequence 6, Application US/08634562
GENERAL INFORMATION:

APPLICANT: Coy, David H.
APPLICANT: Cornish, Jillian
APPLICANT: Reid, Ian Reginald
APPLICANT: Cooper, Garth J.S.
TITLE OF INVENTION: TREATMENT OF BONE DISORDERS
TITLE OF INVENTION: WITH ADRENOMEDULLIN
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,562
FILING DATE: 18-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

```
; BILLING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsao, Y. Rocky
; REGISTRATION NUMBER: 34,053
; REFERENCE/DOCKET NUMBER: 08987/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-634-562-6

Query Match      100.0%; Score 163; DB 10; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.7e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 31
   |||||
Db 8 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 38

RESULT 8
US-08-634-562-11
; Sequence 11, Application US/08634562
; GENERAL INFORMATION:
; APPLICANT: Coy, David H.
; APPLICANT: Cornish, Jillian
; APPLICANT: Reid, Ian Reginald
; APPLICANT: Cooper, Garth J.S.
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS
; TITLE OF INVENTION: WITH ADRENOMEDULLIN
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/634,562
; FILING DATE: 18-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsao, Y. Rocky
; REGISTRATION NUMBER: 34,053
; REFERENCE/DOCKET NUMBER: 08987/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-634-562-11

Query Match      100.0%; Score 163; DB 10; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.8e-17;

; BILLING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Tsao, Y. Rocky
; REGISTRATION NUMBER: 34,053
; REFERENCE/DOCKET NUMBER: 08987/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-634-562-6

Query Match      100.0%; Score 163; DB 10; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.7e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 31
   |||||
Db 8 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 38

RESULT 9
PCT-US02-22821-2
; Sequence 2, Application PC/TUS0222821
; GENERAL INFORMATION:
; APPLICANT: HK Pharmaceuticals, Inc.
; APPLICANT: Kolster, Hubert
; APPLICANT: Siddiqi, Suhail
; APPLICANT: Little, Daniel
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; FILE REFERENCE: 24743-2305
; CURRENT APPLICATION NUMBER: PCT/US02/22821
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 60/306,019
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/314,123
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/363,433
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo Sapien
; PCT-US02-22821-2

Query Match      100.0%; Score 163; DB 1; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 31
   |||||
Db 22 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 52

RESULT 10
US-09-623-548A-935
; Sequence 935, Application US/09623548A
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibodeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 935
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-935

Query Match 100.0%; Score 163; DB 20; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
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Db 22 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 52

RESULT 11

US-09-657-276-935
; Sequence 935, Application US/09657276
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 935
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-935

Query Match 100.0%; Score 163; DB 20; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
|||||
Db 22 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 52

RESULT 12

US-09-813-345-14
; Sequence 14, Application US/09813345
; GENERAL INFORMATION:
; APPLICANT: Smith, Derek D.
; APPLICANT: Saha, Shankar
; APPLICANT: Abel, Peter W.
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Muelling, Raasch & Gebhardt, P.A.
; STREET: 119 North Fourth Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55401
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,345
; FILING DATE: 20-Mar-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: McCormack, Myra H
; REGISTRATION NUMBER: 36,602
; REFERENCE/DOCKET NUMBER: 180.00020101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/305-1220
; TELEFAX: 612/305-1228

; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 52 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-813-345-14

Query Match 100.0%; Score 163; DB 23; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
|||||
Db 22 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 52

RESULT 13

US-10-197-954-2
; Sequence 2, Application US/10197954
; GENERAL INFORMATION:
; APPLICANT: K*ster, Hubert
; APPLICANT: Siddiqi, Suhail
; APPLICANT: Little, Daniel
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2305
; CURRENT APPLICATION NUMBER: US/10/197,954
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 60/306,019
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/314,123
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/363,433
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; TYPE: PRT
; LENGTH: 52
; ORGANISM: Homo Sapien
US-10-197-954-2

Query Match 100.0%; Score 163; DB 27; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 31
|||||
Db 22 TVQKLAHQIYQFTDKDKNVAPRSKISPGY 52

RESULT 14

US-10-360-101-74
; Sequence 74, Application US/10360101

```
; GENERAL INFORMATION:
; APPLICANT: Moll, Gert N.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10/360,101
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A13,S16-sequence of Adrenomedullin Hypotensive peptide
US-10-360-101-74
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Query Match      100.0%; Score 163; DB 29; Length 52;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 31
      |||||||
Db      22 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 52
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RESULT 15
US-09-724-676-63615
; Sequence 63615, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63615
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-63615
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Query Match      100.0%; Score 163; DB 21; Length 113;
Best Local Similarity 100.0%; Pred. No. 7.1e-17;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 31
      |||||||
Db      44 TVQKLAHQIYQFTDKDKDNVAPRSKISPGY 74
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Search completed: October 14, 2003, 08:51:05
Job time : 406.114 secs